

Modifications / Engineering:

- 1.) Séparate Intein Domains (designated A and B)
- 2.) Reverse Translational Order
- 3.) Fuse Former C and N-termini

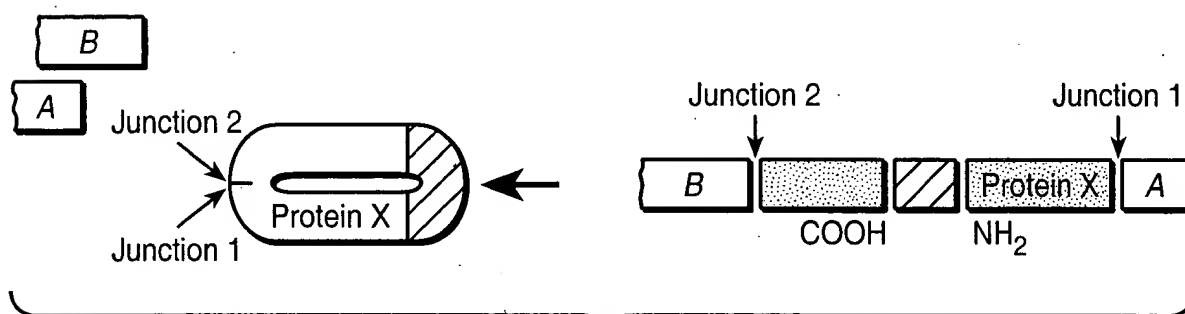
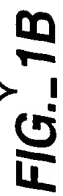


FIG. 1A



3 / 52

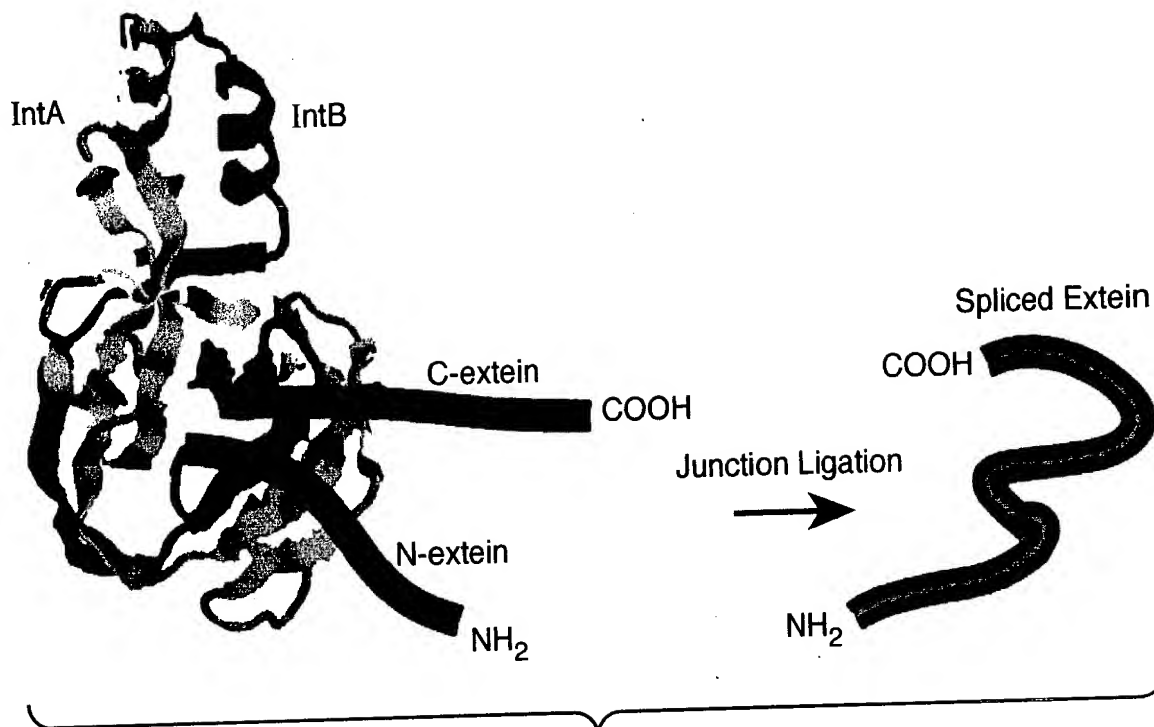


FIG._2A

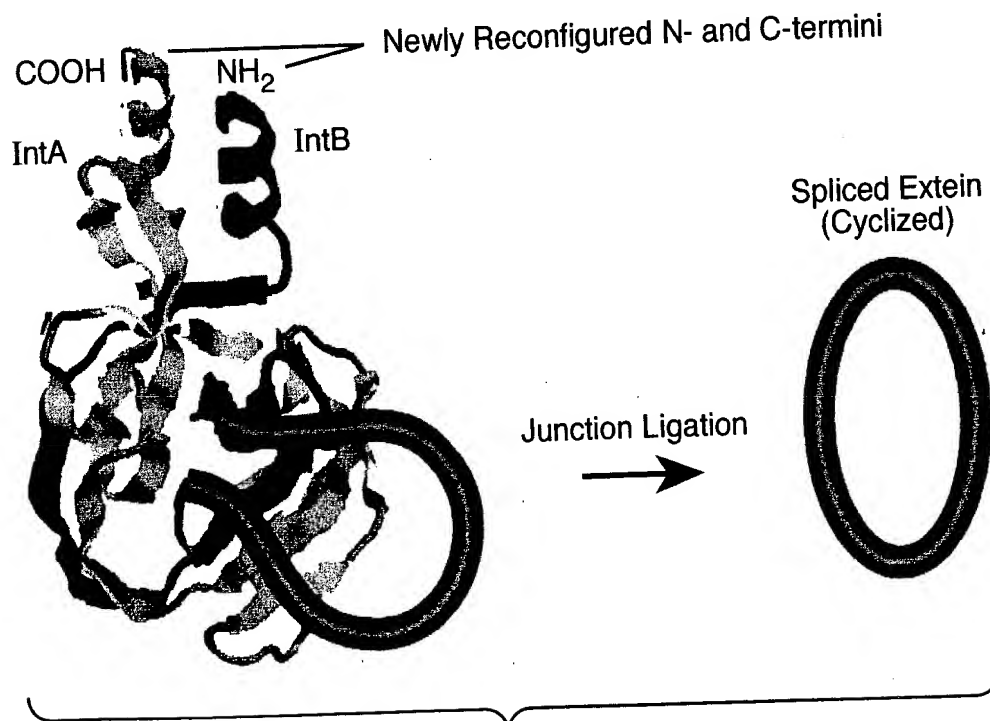


FIG._2B

GCISGDSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLES AKVSRVFCTGKKLVYILKT
RLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLMSDEELGLLGHLIGDGC
TLPRHAIQYTSNKIELAEKVVELAKAVFGDQINPRISQERQWYQVYIPASYRLTHNKNPIT
KWLENLDVFGRLRSYEKFVPNQVFEQPQRAIAIFLRHLWSTDGCVKLIVEKSSRPVAYYATSS
EKLAQDVQSLLLKLGINARLSKISQNGKGRDNYHVTITGQADLQIFVDQIGAVDKDKQASVE
EIKTHIAQHQAQNTNRDVIPKQIWKTYVLPQIQIKGITTRDLQMR LGNAYCGTALYKHNL SRE
RAAKIATITQSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVANDIIVHNS

FIG._3A

YCITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNPVLADRLFHSGEHPVYTV
RTVEGLRVTGTANHPLLCLVDVAGVPTLLWKLIDEIKPGDYAVIQRSASFVDCAGFARGKPE
FAPTTYTVGVPGLVRFLEAHHRDPDAQIADELTDGRFYAKVASVTDAGVQPVYSLRVDTA
DHAFITNGFVSHNT

FIG._3B

ECLTSDHTVLTTTRGWIP IADVTLDDKVAVL DNNTGEMSYQNPQKVHKYDYEGPMYEVKTAGV
DLFVTPNHRMYVNTTNNTTNQYNLVEASSIFGKKVRYKNDAIWNKTDYQFILPETATLTGH
TNKISSTPAIQPEMNAWLTFGLWIANGH TTKIAEKTAENNQKQRYKVILTQVKEDVCDII
EQTLNKLGFNFIRSGKDYTIENKQLWSYLNPF DN GALNKYLPDWVWELSSQCKILLNSLCL
GNCLFTKNDDTLHYFSTSERFANDVSRLALHAGTTSTIQLEAAPS NLYDTIIGLPVEVNTTL
WRVIINQSSFYSYSTDKSSALNLSNNVACYVNAQSALTLEQNSQKINKNTLVLTKNNVKSQT
MHSQRAERVD TALLTQKELDNSLNHEILINKNPGTSQLECVVNPEVNNTSTNDRFVYYKGPV
YCLTGPNNVFYVQRNGKAVWTGNS

FIG._3C

LCVAPETMILTEDGQFP IKDLEGKIIKVWNGNEFSSVTVVKTGTEKELLEVE LSNGCTL SCT
PEHKFIIVKSYTEAKKQKTDDNAIANAERVDAQDLKPRMKLIKFDLPTLFGNSEHDIKYPYT
HGFFCGDGTYTKYGKPKQLSLYGDKKELTYLDVRTMTGLE DASGR LNTWLPLDLAPKFDVPI
NSSLECRM EWLAGYLDADGCVFRNGT NESIQVSCIHLDFLKRIQLLLIGMGVTSKITKLHDE
KITTMPDGKGGQKPYSCKPIWRLF ISSGLYHLSEQGFETRRLKWEPRQPQRNAERFVEVLK
VNKTGRVDDTYCFTEPINHAGVFNGILTQC

FIG._3D

GCFTKGTQVMMADGADKSIESIEVGDKVMGKDGM PREVVGLPRGYDDMYKVRQLSSTRNAK
SEGLMDFTVSADHKLILKTKQDVKIATR KIGNTYTGVTFYVLEKTKTGIELVKAKTKVFGH
HIHGQNGAE EKAATFAAGIDSKEYIDWII EARDYVQVDEIVKTSTTQMINPVHFESGKLGW
LHEHKQNKSLAPQLGYLLGTWAGIGNVKSSAFTMNSKDDVKLATRIMNYSSKLGMTCSSTES
GELNVAENEEFFNNLGAEKDEAGDFTFDEFTDAMDELTINVHGA AASKKNLLWNALKSLG
FRAKSTDIVKSIPQHIAVDDIVVRESLIAGLVDAAGNVETKSNGSIEAVVRTSFRHVARGLV
KIAHSLGI ESSINIKDTHIDAAGVRQEFACIVNLTGAPLAGVLSKALARNQTPVVKFTRDP
VLFNFDLIKSAKENYYGITLAEETD HQFLLSNMALVHNC

FIG._3E

GCLSYATNQPYFLKSDNVNFSKLTSLKVSNNHYILSATLELLIPFQYNRIYPIVSLIKRELQT
GYKVVEYELDFYISVIVSTVEHYVLTNGWKRIELTVDLVDATLDIQYLIYNNTEVDLFSSN
VIFSSVINLICMNRINVYDFWIPKTNNFFVNALLVHNS

FIG._3F

GCISKFSHIMWSHVSKPLFNFSIKKSHMHNFNKNIYQLLDQGEAFISRQDKKTTYKIRTNSE
KYLELTSNHHKILTLRGWQRCDQLLCNDMITTQIGFELSRRKKYLLNCIPFSLCNFETLANIN
ISNFQNVFDFAANPIPNIANNIIVHNS

FIG._3G

GCFAGKTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPGRGRETMYSVVQKSQHRAHKS
DSSREVPPELLKFTCNATHELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVELV
KEVSKSYPISEGPERANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAPILYE
NDHFFDYMQSKSFHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTEYAEKLN
LCAEYKDRKEPQVAKTVNLYSKVVRGNGIRNNLNNTENPLWDAIVGLGFLKDGKVNIPSFLST
DNIGTRETFLAGLIDSDGYVTDEHGKATIKTIHTSVRDGLVSLARSLGLVSVNAEPAKVD
MNGTKHKISYAIYMSGGDVLLNVLSKAGSKKFRPAPAAFARECRGFYFELQELKEDDYG
ITLSDSDHQFLLANQVVVHNC

FIG._3H

GCFAYGTRGALADGTTEKIGKIVNQKMDVEVMSYDPDQVVPKVVNWFNNGPAEQFLQFT
VEKSGGNGKSQFAATPNHLIRTPAGWTEAGDLVAGDRVMAAEPHRLSDQQFQVVLGSLMGDG
NLSPNRRDRNGVRFRMGHGAKQVDYLQWKTALLGNIKHSTHVNDKGATFVDFTPLELAELQ
RAVYLGDGKKFLSEENFKALTPLALVFWYMDGPFVTRSKGLQERTAGGSGRIEICVEAMSE
GNRIRLRDYLDRDTHGLDVRLRLSGAAGKSVLVFSTASSAKFQELVAPYITPSMEYKLLPRFR
GQGAVTPQFVEPTQRLVPARVLDVHVKPHTRSMNRFDIEVEGNHNYFVDGVMVHNS

FIG._3I

YCLSFGTEILTVEYGPLPIGKIVSEEINCSVYSVDPEGRVYTQAIQWHDGRGEQEVLEYELE
DGSVIRATSDHRFLTDDYQLLAIEEIFARQLDLLTLENIKQTEEALDNHRLPFPLLDAGTIK

FIG._3J

KALALDTPLPPTGTAMGDVAVGDELLAVDEAPTRVVAATEVMLGRPCYEIEFSDGTVIVA
DAQHQWPTSYGIRTSQALRCGLDIIAAAGSTPRHAGRLTTAAAFMAPVLCIDSVRRVRSVPVR
CVEVDNAAHLYLAGRGMVPTHNS

FIG._3K

GALAYDEPIYLSDGNIINIGEFVDKFFKKYKNSIKKEDNGFGWIDIGNENIYIKSFNKLSLI
IEDKRILRVWRKKYSGKLIKITTNRREITLTHDHPVYISKTEGVLEINAEMVKVGDIYIIP
KNNTINLDEVIKVETVDYNGHIYDLTVEDNHTYIAGKNEGFAVSNC

FIG._3L

GALYDFSVIQLSNGRFVLIGDLVEELFKKYAEKIKTYKDLEYIELNEEDRFEVVSVPD1KA
 NKHVVSrvWRRKvREGKLiRIKTRTGNEIILTRNHPLFAFSNGDVVRKEAEKLVGDRVAV
 MMRPPSPQTKAVVDPaiYVKISDYyLVpNGKGMiKVPNDGIPPEKAQYLLSVNSYPVKLVR
 EVDEKLSYLAGVILGDGYISSNGYYISATFDDEAYMDAFVSVVSDfIPNYVPSIRKNGDYTI
 VTVGSKIFAEMLSRIFGIPRGRKSMWDIPDVVLSNDDLMRYFIAGLFDADGYVDENGPSIVL
 VTKSETVARKIWIYVLQRlGIISTVSRVKSrGFKEGELFRViiSGVEDLAKFAKFIPLRHSRK
 RAKLMEILRTKKPYRGRRTYRVPISSDMIAPLRQMLGLTVAELSKLASYYAGEKVSESLIRH
 IEKGRVKEIRRSTLKGIALALQQIAKDVGNEEAWVRakRLQlIAEGDVYWDEVVSVEEVDPK
 ELGIEYVYDLTVEDDHNYVANGILVSNc

FIG._3M

PCVSGDTIVMTSGGPRTVAEELEGKPFTALIRGSGYPCPSGFFRTCERDVYDLRTREGHCLRL
 THDHRVLVMDGGLEWRAAGELERGDRVLVMDDAAGEFPALATFRGLRGAGRQDVYDATVYGAS
 AFTANGFIVHNC

FIG._3N

GCIDGKAKIIIFENEgeehLTtMEemyERYKHLGEfyDEEYNRWGIDVSNVPIYVKSFDPEsk
 RVVKGKVNVIWKYELGKDVTkyEiiTNKGTKILTSPWHPFFVLTPDFKIVEKRADELKEGDI
 LIGGMPDGEDYKFIFDYWLAGFIAGDGCfDKYHSHVKGHEyIYDRLRIYDYRIETFEIINDY
 LEKTFGRKYSIQKDRNIYYIDIKARNITSHYLKLLEGIDNGIPPQILKEGKNAVLsFIAGLF
 DAEGHVSNKPGIELGMVNKRLIEDVTHYLNALGIKARIREKLrKDGIDYVLHVEEYSSLLRF
 YELIGKNLQNEEKREKLEKVLsnHKGNfGLPLNFNAfKEWASEYGVefKTNGSQTIAIIND
 ERISLGQWHTRNRVSKAVLVKMLRKLyeATKDEEVKRMLHLIEGLEVVrHITTTNEPRTfyD
 LTVENYQNYLAGENGMIfvHNT

FIG._3O

NSILPEEWVPLIKNGKVKIFRIGDFVDGLMkanQGKVKKTGDTEVLEVAGIHAFsFDRKSKK
 ARVMAVKAVIRHRYSGNVYRIVLNSGRKITITEGHSLFVYRNGDLVEATGEDVKIGDLLAVP
 RSVNLPEKRERLNIVELLLNLSPEETEDIILTIPVKGRKNFFKGMLRTLrWIFGEEKRVRTA
 SRYLRHLENLGYIRLRKIGYDIIDKEGLEKYRTLYEKLVDVVRyNGNKREYLVEFNAVRDVI
 SLMPEEELKEWRIGTRNGFRMGTFVDIDEDfAKLLGYyVSEGSARKWKNQTGGWSYTVRLYN
 ENDEVLDDMEHLAKKFFGKVKGKNYVEIPKkMAYIIFESLCGTlaENKRVPEVIFTSSKGV
 RWAfLEGYfIGDGDVHPskRVRLSTKSELLVnGLVLLLNSLGVSAIKLGYDSGVYRVYVNEE
 LKFTEYRKKKNVYHSHIVPKDILKETFGKVFQKNISYKKfRELvENGKLDREKAKRIEWLLN
 GDIVLDRVVEIKREYYDGYVYDLSVDEDENfLAGFGfLYAHNS

FIG._3P

DSVTGETETIIIKRNGKVEFVAIEELFQRVDIRIGEKEYCVLEGVEALTLDNRGRLVWKSVPY
VMRHRTNKRIYRVWFTNSWYLDVTEHDHSLIGYMNTSKVKPGKPLKERLVEVKPGELGESVKS
LITPNRAIAHGIRVNPPIAVKLWELIGLLVGDGNWGGQSNWAKYNVGLSLGLDKEEIEEKILK
PLKNTGIIISNYDYKSKKGDVSILSKWLARFMVRYFKDESGSKRIPEFMFNLPREYIEAFLRG
LFSADGTVSLRKGVPVRLTSVNPELSSSVRKLLWLVGVSNSMFVETNPNRYLGKESGTHSV
HVRIKDKHRFAERIGFLLDRKATKLSNENLGHTSKKRAYKYDFDLVYPKKVEEIAYDGYVYD
IEVEGTHRFFANGILVHNT

FIG._3Q

KCLLPEEKVVLPEIGLVTLRELFELANEVVVKDEEKEVRKLGKMLTGVDERGNVKLLNALYV
WRVAHKGEMIRVKVNGWYSVTVTPEHPFLTNRGWVKAGELKEGDYIAIPRRVYGNEDIMKFS
KIAKELGIKGDEKEFYLAGASLDIPIKVLFLAPSKLVSAFLRGYFDAKGVVRENYIEVPLFE
DLPLLLLRFGIVSRIEKSTLKISGKRNLLEFRKHVGFTDSEKAKALDELISKAKESERYPII
EELRRLGLLFGFTRNELRIEENPTYEVIMEILERIERGSPNLAEKIAVLEGRIKEENYLRL
EEEGLIENGLTELKELLEVRNREFDSKDVDYVRNIVENLVFLPVEKVERIEYEGYVYDV
TTETHNFVANGILVHNT

FIG._3R

QCFSGEEVIIVEKGKDRKVVKLREFVEDALKEPSGEGMDGDIKVTYKDLRGEDVRILTKDGF
VKLLYVNKREGKQQLRKIVNLDKDYWLAVTPDHKVFTSEGLKEAGEITEKDEIIRVPLVILD
GPKIASTYGEDGKFDDYIRWKKYEKTGNGYKRAAKELNIKESTLRWWTQGAKPNSLKMIEE
LEKLNLLPLTSEDSRLEKVAIILGALFSDGNIDRNFNTLSFISSEKAIERFVETLKELFGE
FNYEIRDNHESLGKSILFRTWDRRIIRFFVALGAPVGNKTKVKLELPWWIKLKPSLFLAFMD
GLYSGDGSVPRFARYEEGIKFNGTTEIAQLTDDVEKKLPFFEEIAWYLSFFGIKAKVRVDKT
GDKYKVRLLFSQSIDNVNLFLEFIPISLSPAKREKFLREVESYLAAPPESSLAGRIEELREH
FNRIKKGERRSFJETWEVVNVNTYNVTTETGNLLANGLFVKNS

FIG._3S

LCLTPDTYVVLGDGRIETIEDIVNAKERNVLSLDLDNLSIKIDTAIKFWKLRYNGNLSKITL
SNNYELKATPDHCLLVLRDNQLKWIPAKDIKENDYIAMPFNYKVERKPIISLLNLLKYLDITD
VLIEFDENSTIFEKIAEYIRNNIKTSTKYKYLRNRRVPLKYLIEWNFDLDEIEKEAKYIYKS
VAGTKKIPLFKLDERFWYFAGLVLGDSIQDSKIRIAQTPLKDVKSILDETFFPLHNWISGN
QVIISNPIIAEILEKLGMRNGKLNIGIIFSLPESYINALIAGYFDTDGCFSLLYDKKAKKHNL
RMVLTSKRRDVLEKIGIYLN SIGILNTLHKSREVYSLIISNKSLET FKEKIAKYLKIRKEAF
INGYKTYKKEHEERFECDLLPVKEVFKLTFEKGRKEILKDSKIHENWYKEKTNNIPREKL
KTVLRYANNSEHKEFLEKIVNGDISFVRVKKVENIPYDGYVYDLSIKHNQNFISNGVISHNC

FIG._3T

KCLTGDTKVIANGQLFELRELVEKISGGKFGPTPVKGLKVGIGIDEDGKLREFEVQYVYKDKT
 ERLIRIRTRLGRELKVTPYHPLLNNRRNGEIKWVKAELKPGDKLAVPRFLPIVTGEDPLAE
 WLGYFLGGGYADSKENLIMFTNEDPLLQRQFMELTEKLFSDARIREITHENGTSKVYVNSKK
 ALKLVNSLGNNAHIPKECWRGIRSFRLRAYFDCNGGVKGNAIVLATASKEMSQEIAYALAGFGI
 ISRIQEYRVIIISGSDNVKKFLNEIGFINRNKLEKALKLVKKDDPGHDGLEINYELISYVKDR
 LRLSFFNDKRSWSYREAKEISWELMKEIYYRLDELEKLKESLSRGILIDWNEVAKRIEEVAE
 ETGIRADELLEYIEGKRKLSFKDYIKIAKVLGIDVEHTIEAMRVFARKYSSYAEIGRRLGTW
 NSSVKTILESNAVNVEILERIRKIELELIEEILSDEKLKEGIAYLIFLSQNELYWDEITKVE
 ELRGEFIIYDLHVPGYHNFIAGNMPTVVHNT

FIG._3U

SCVTGDTKVYTPDEREVKIRDFMNYFENGLIKEVSNRIGRDTVIAAVSFNSRIVGHPVYRLT
 LESGRIIEATGDHMFALTPEGWKQTYDIKEGSEVLVKPTLEGTPYEPDPRVIIDIKEFYNFLE
 KIEREHNKPLKEAKTFRELITKDKEKILRRALELRAEIEGLTKREAEILELISADTWIPR
 AELEKKARISRTRLNQILQRLEKKGYIERRIEGRKQFVRKIRNGKILRNAMDIKRILEEEFG
 IKISYTTVKLLSGNVDMAYRILKEVKEKWLVRDDEKAGILARVVGFIILGDGHLARNRI
 WFNSSKEELEMLANDLRKLGLKPSEIIERDSSSEIQGRKVKGRIYMLYVDNAAFHALLRFWK
 VEVGNKTKGYTVPEWIKGNLFBKREFLRGLFGADGTPCKGKRYNFGIKLEIRAKKESLE
 RTVEFLNDVADLLREFDVDISKITVSPTKEGFIIRLIVTPNDANYLNFLTRVGYAYAKDTYAR
 LVGEYIRIKLAYKNIILPGIAEKAIELATVTNSTYAAKVLGVSRDFVVRNLKGTQIGITRDF
 MTFEEFMKERVNLNGYVIEKVIKKEKLGYLVDVYDVT CARDHSFISNGLVSHNC

FIG._3V

NCLTSNSKILTDDGYIYKLEKLKEKLDLHIKIYNTTEEKSSNILFVSERYADEKIIRIKTE
 SGRVLEGSKDHPVLTNLNGYVPMGMLKEGDDVIVYPYEGVEYEEPSDEIILDEDDFAEYDKQI
 IKYLDKDRGLLPLMDNKNIGIIRALLGFAFGDGSIVKENDRERLYVAFYGKRETLIKIREN
 LEKLGIKASRIYSRKREVEIRNAYGDEYTSLCDNSIKITSKAFALFMHKLGMPIGKKTEQI
 YKIPewIKKAPKWVRNFLAGLFGADGSRAVFKNYTLPINLTMSKSEELKENILEFLNEIK
 LLLAEFDIESMIYEIKSLDGRVSYRLAIVGEESIKNFLGRINYEYSGEKKVIGLLAYEYLR
 KDIAKEIRKKCIKRAKELYKKGVTVSEMLKMDFRNEFISKRLIERAVYENLDEDDVRISTK
 FPKFEEFIEKYGVIGGFVIDKIKEIEEISYDSKLYDVGVISKEHNFANSIVVHNC

FIG._3W

KCVDGDTLVLTKEFGLIKIKELYEKLDGKGRKIVEGNEEWTELEKPITVYGYKDGKIVEIKA
 THVYKGVSSGMVEIRTRTGRKIKVTPIHRLFTGRVTKDGLILKEVMAMHVKPGDRIAVVKKI
 DGGEYIKLDSSNVGEIKVPEILNEELAEFLGYLMANGTLKSGIIEIYCDDESLLERVNSLSL
 KLFGVGGRIVQKVDGKALVIQSKPLVDVLRRLGVPEDKKVENWKVPRELLSPPSNVVRAFVN
 AYIKGKEEVEITLASEEGAYELSYLFAKLGIVYVTSKSGEYKVRVSRRGNLDTIPVEVNGM
 PKVLPYEDFRKFAKSIGLEEVAENHLQHIIIFDEVIDVRYIPEPQEVYDVT TETHNFVGGNMP
 TLLHNT

FIG._3X

MESG[SPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVAND

I	I	V	H	N	S	I	E	Q	G	Q	G	G	M	S	M	D	Y	K	D	D	D	K	M	R	M	L	E	G	Q	A	G	G	L	I	T	S	G	C	I	S
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

GDSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLESKVS RVFCT

GKKLVYILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRK

LESSSLQLSINGYH

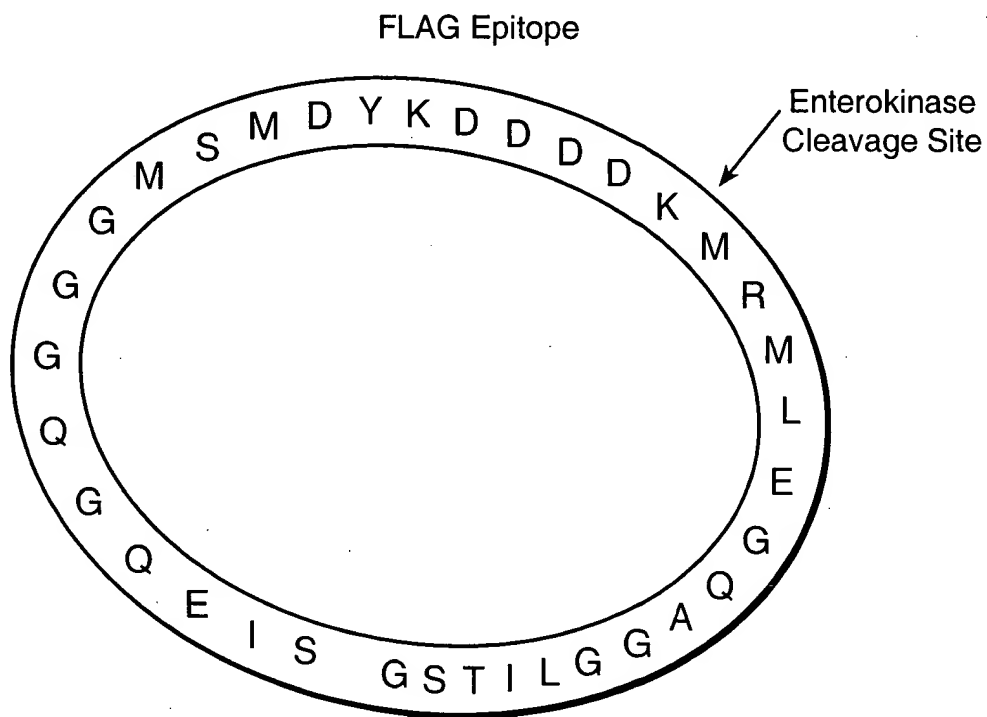


FIG. 4A

CMV Promoter →

1 / 1	GCT	TGG	CGA	TGT	ACG	GGC	CAG	ATA	TAC	GCG	TTG	ACA	TTG	ATT	ATT	GAC	TAG	TTA	TTA	ATA
121 / 41	TAC	GGT	AAA	TGG	CCC	GCC	TGG	CTG	ACC	GCC	CAA	CGA	CCC	CCG	CCC	ATT	GAC	GTC	AAT	AAT
241 / 81	TTT	ACG	GTA	AAC	TGC	CCA	CTT	GGC	AGT	ACA	TCA	AGT	GTA	TCA	TAT	GCC	AAG	TAC	GCC	CCC
361 / 121	GGA	CTT	TCC	TAC	TTG	GCA	GTA	CAT	CTA	CGT	ATT	AGT	CAT	CGC	TAT	TAC	CAT	GGT	GAT	GCG
401 / 161	CCA	CCC	CAT	TGA	CGT	CAA	TGG	GAG	TTT	GTT	TTG	GCA	CCA	AAA	TCA	ACG	GGA	CTT	TCC	AAA
601 / 201	CTA	TAT	AAG	CAG	AGC	TCT	CTG	GCT	AAC	TAG	AGA	ACC	CAC	TGC	TTA	CTG	GCT	TAT	CGA	AAT
721 / 241	CTG	tcg	act	GGA	GGA	ACC	ATG	GAG	TCC	GGA	tca	cca	gaa	ata	gaa	aag	ttg	tct	cag	agt
841 / 281	ttg	act	gtg	cca	gga	cca	cat	aac	ttt	gtc	gcc	aat	gac	atc	att	gtc	cat	aac	aat	aat
961 / 321	ATG	ctc	gag	ggc	caa	gca	ggc	gga	CTG	ATC	ACC	agt	ggc	ATC	AGT	GGA	GAT	AGT	ttg	ttg
1081 / 361	ttt	gaa	ata	tgg	gca	att	aat	gaa	cag	acg	atg	atg	atg	cta	gaa	tca	gct	aaa	gtt	agt
1201 / 401	aag	gca	aca	aat	cat	aga	ttt	tta	act	act	att	gat	ggc	ggt	aaa	aga	aga	ttt	gat	gag
1321 / 441	GAT	cca	tgg	tta	cca	TGA	caa	ttg	GCG	GCC	GCT	CGA	GTC	TAG	AGG	GCC	CGC	GGT	TCG	AAG
1441 / 481	ATC	ACC	ATT	GAG	TTT	AAA	CCC	GCT	GAT											

FIG. 4B-1

61 / 21	GTA ATC AAT TAC GGG GTC ATT AGT TCA TAG CCC ATA TAT GGA GTT CCG CGT TAC ATA ACT	91 / 31
181 / 61	GAC GTA TGT TCC CAT AGT AAC GCC AAT AGG GAC TTT CCA TTG ACG TCA ATG GGT GGA CTA	211 / 71
301 / 101	TAT TGA CGT CAA TGA CGG TAA ATG GCC CGC CTG GCA TTA TGC CCA GTA CAT GAC CTT ATC	331 / 111
421 / 141	GTT TTG GCA GTA CAT CAA TGG GCG TGG ATA GCG GTT TGA CTC ACG GGG ATT TCC AAG TCT	451 / 151
541 / 181	ATG TCG TAA CAA CTC CGC CCC ATT GAC GCA AAT GGG CGG TAG GCG TGT ACG GTG GGA GGT	571 / 191
661 / 221	TAA TAC GAC TCA CTA TAG GGA GAC CCA AGC TGG CTA GTT AAG CTT cct ata cta gga GAT	691 / 231
781 / 261	gat att tac tgg gac tcc atc gtt tct att acg gag act gga gtc gaa gag gtt ttt gat	811 / 271
901 / 301	IntB (Ic)	
901 / 301	Flag Epitope Insert 931 / 311	
1021 / 341	GAA CAA ggc cag ggc ggc ATG TCA ATG gac tat aaa gat gac gat aag ATG AGG	1051 / 351
1141 / 381	IntA (IN)	1171 / 391
1261 / 421	gta ttt tgt act ggc aaa aag cta gtt tat att tta aaa act cga cta ggt aga act atc	1291 / 431
1381 / 461	tct tta aaa gag cat att gct cta ccc cgt aaa cta gaa agc tcc tct tta caa tta ATC	1411 / 471
	GTA AGC CTA TCC CTA ACC CTC TCC TCG GTC TCG ATT CTA CGC GTA CCG GTC ATC ATC ACC	

FIG..4B-2

FIG..4B

FIG..4B-1

FIG..4B-2

ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT
 CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGGATTTGACTGTGCCAGGGCCCCATA
 ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGACG
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCCAACGAGAAGCGCGATCACATGG
 TCCTGCTGGAGTTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG
 TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC
 CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC
 GGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGACGTGCTT
 CAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCGAAGGCT
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA
 CGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATCATGG
 CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACCTC
 GAGCAAAAGCTGATATGCATCTCCGGAaATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG
 AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA
 CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT
 ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT
 TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC
 TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC
 GCTATCGATTAA

FIG._5A

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG
 SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT
 GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV
 KFEGLTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL
 EQKLICISGNSLISLASTGKRVSIDLLDEKDFEIWAINETMKLESASVSRVFCTGKKLVY
 ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY
 AIDZ

FIG._5B

ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT
 CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGGATTTGACTGTGCCAGGGCCCCATA
 ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGGCAGCGGCCCCGTGCTGCTGCCCGACAA
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCCAACGAGAAGCGCGATCACATGG
 TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG
 TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC
 CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC
 GGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT
 CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA
 TGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCATC
 GTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGGATTTGACTGTGCCAGGGCCCCATAA
 CTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAGC
 TCGCCGACCACTACCAGCAGAACACCCCCATCGGGCAGCGGCCCCGTGCTGCTGCCCGACAA
 CACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCCAACGAGAAGCGCGATCACATGGT
 CCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGGT
 CGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTACC
 GGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC
 CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC
 GCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCCTGACCTACGGCGTGCAGTGCTTC
 AGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTA
 CGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGA
 AGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGAC
 GGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCATGGC
 CGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACCTCG
 AGCAAAAGCTGATATGCATCTCCGGAAATAGTTTGATCAGCTTGCGCAGCACAGGAAAAAGA
 GTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGAC
 GATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAGCTAGTTTATA
 TTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAaATTTTAACTATT
 GATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAAGAGCATATTGCTCTACCCCGTAACT
 AGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCTACGACGTCCCGGACTACG
 CTATCGATTAA

FIG._5C

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG
 SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT
 GKLPVPWP TLVTTLTYGVQCF SRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRA EV
 KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL
 EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLESAKVS RVFCTGKKLVY
 ILKTRLGRTIKATANHKFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY
 AIDZ

FIG._5D

ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT
 CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA
 ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG
 TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG
 TCGAACGGGGGAATTCTCGCAGGTAGACAAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTCAC
 CGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC
 GGCAAGCTGCCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT
 CAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCGAAGGCT
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA
 CGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGG
 CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACCTC
 GAGCAAAAGCTGATATGCATCTCCGGAaATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG
 AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCagTTAATGAACAGA
 CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT
 ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT
 TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC
 TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC
 GCTATCGATTAA

FIG._5E

MESGSPEIEKLSQSDIYWDSIVSITETGVVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG
 SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT
 GKLPVPWPTLVTTLTYGVCQFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV
 KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL
 EQKLICISGNSLISLASTGKRVSIDLLDEKDFEIWAVNEQTMKLESASVSRVFCTGKKLVY
 ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY
 AIDZ

FIG._5F

ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT
 CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGgCcGTGCCAGGGCCCCATA
 ACTTTGTGGCCAATGACATCATTTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCGAG
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG
 TCCTGCTGGAGTTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG
 TCGAACGGGGAAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC
 CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC
 GGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCGAGTGCTT
 CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCT
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA
 CGGCAACATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGG
 CCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGACCTC
 GAGCAAAAGCTGATATGCATCTCCGAAATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG
 AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA
 CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT
 ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT
 TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC
 TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC
 GCTATCGATTAA

FIG._5G

MESGSPEIEKLSQSDIYWDSIVSITETGVVEEVFDLAVPGPHNFVANDIIVHNSEEDLGSSVQ
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG
 SNGEFSQVDKSMVSKGEELFTGVVPILEVELDGDVNGHKFSVSgegeGdatYgKLTLKFICTT
 GKLPVPWPTLVTTLTyGVQCFsRYPDHMKQHDFfKSAMPEGYVQERTIFFKDDgNYKTRAeV
 KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNshNVYIMADKQKNGIKVNFkIRHNIEDL
 EQKLICISGNSLISLASTGKRVSIKDLLDEKDFEIWAINeqTMKLESAKVSrVfCTGKKLVY
 ILKTRLGRTIKATANHRFLtIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY
 AIDZ

FIG._5H

ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT
 CGTTcCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGGATTTGACTGTGCCAGGGCCCCATA
 ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCGAG
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG
 TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG
 TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC
 CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC
 GGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCGAGTGCTT
 CAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCGAAGGCT
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA
 CGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCATGG
 CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACCTC
 GAGCAAAAGCTGATATGCATCTCCGGAaATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG
 AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA
 CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT
 ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT
 TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC
 TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC
 GCTATCGATTAA

FIG._5I

MESGSPEIEKLSQSDIYWDSIVPITETGVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG
 SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT
 GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV
 KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL
 EQKLICISGNSLISLASTGKRVSIDLLDEKDFEIWAINETMKLESASVSRVFCTGKKLVY
 ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY
 AIDZ

FIG._5J

ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT
 CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA
 ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCCAACGAGAAGCGCGATCACATGG
 TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG
 TCGAACGGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC
 CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC
 GGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT
 CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA
 CGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATCATGG
 CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACCTC
 GAGCAAAAGCTGATATGCATCTCCGGAAATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG
 AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA
 CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAGGCTAGTTTAT
 ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT
 TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC
 TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC
 GCTATCGATTAA

FIG._5K

MESGSPEIEKLSQSDIYWDSIVSITETGVVEEVDLTVPGPVPHNFVANDIIVHNSEEDLGSSVQ
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG
 SNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT
 GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV
 KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDL
 EQKLICISGNSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLESAKVS RVFCTGKRLVY
 ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY
 AIDZ

FIG._5L

ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT
 CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGGATTTGACTGTGCCAGGGCCCCATA
 ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGACG
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCCAACGAGAAGCGCGATCACATGG
 TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG
 TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC
 CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC
 GGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT
 CAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCC GAAGGCT
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA
 CGGCAACATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGG
 CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACCTC
 GAGCAAAAGCTGATATGCATCTCCGGAGATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG
 AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA
 CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT
 ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAAATTTTAACTAT
 TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC
 TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCTACGACGTCCCGGACTAC
 GCTATCGATTAA

FIG._5M

MESGSPEIEKLSQSDIYWDSIVSITETGVVEEFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG
 SNGEFSQVDKSMVSKGEELFTGVVPILEVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT
 GKLPVPWPFTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV
 KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDL
 EQKLICISGDSLISLASTGKRVS IKDLLDEKDFEIWAIN EQTMKLESAKVS RVFCTGKKLVY
 ILKTRLGRTIKATANHKFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY
 AIDZ

FIG._5N

ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCA
 CGTTcCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA
 ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG
 CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAA
 CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCCAACGAGAAGCGCGATCACATGG
 TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG
 TCGAACGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTCA
 CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT
 CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC
 GGCAAGCTGCCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTT
 CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT
 ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG
 AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA
 CGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGG
 CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACCTC
 GAGCAAAAGCTGATATGCATCTCCGGAGATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG
 AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAATTAATGAACAGA
 CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTGTACTGGCAAAAAGCTAGTTTAT
 ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT
 TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC
 TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC
 GCTATCGATTAA

FIG._50

MESGSPEIEKLSQSDIYWDSIVPITETGVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ
 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG
 SNGEFSQVDKSMVSKGEELFTGVVPILEVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT
 GKLPVPWPVTLVTTLTYGVQCFSTRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV
 KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDL
 EQKLICISGDSLISLASTGKRVSIDLLDEKDFEIWAINETMKLESASVSRVFC TGKKLVY
 ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY
 AIDZ

FIG._5P

ATGGAGTCCGGATCACCAGAAATAGAAAAGTTGTCTCAGAGTGATATTTACTGGGACTCCAT
CGTTTCTATTACGGAGACTGGAGTCGAAGAGGTTTTTGATTTGACTGTGCCAGGGCCCCATA
ACTTTGTGGCCAATGACATCATTGTCCATAACAGTGAGGAGGACCTGGGATCCAGCGTGCAG
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGGCGACGGCCCCGTGCTGCTGCCCGACAA
CCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCCAACGAGAAGCGCGATCACATGG
TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGGG
TCGAACGGGGGAATTCTCGCAGGTAGACAAGTCGATGGTGAGCAAGGGCGAGGAGCTGTTTAC
CGGGGTGGTGCCATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGT
CCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC
GGCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCCTGACCTACGGCGTGCAGTGCTT
CAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG
AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA
CGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATCATGG
CCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACCTC
GAGCAAAAGCTGATATGCATCTCCGGAGATAGTTTGATCAGCTTGGCGAGCACAGGAAAAAG
AGTTTCTATTAAAGATTTGTTAGATGAAAAAGATTTTGAAATATGGGCAGTTAATGAACAGA
CGATGAAGCTAGAATCAGCTAAAGTTAGTCGTGTATTTTGTACTGGCAAAAAGCTAGTTTAT
ATTTTAAAACTCGACTAGGTAGAACTATCAAGGCAACAGCAAATCATAGATTTTAACTAT
TGATGGTTGGAAAAGATTAGATGAGCTATCTTTAAAGAGCATATTGCTCTACCCCGTAAAC
TAGAAAGCTCCTCTTTACAATTAGGCCTCCGCGGCCAGTACCCCTACGACGTCCCGGACTAC
GCTATCGATTAA

FIG._5Q

MESGSPEIEKLSQSDIYWDSIVSITETGVEEVFDLTVPGPHNFVANDIIVHNSEEDLGSSVQ
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDELYKG
SNGEFSQVDKSMVSKGEELFTGVVPILEVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT
GKLPVPWPTLVTTLTYGVCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEV
KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNShNVYIMADKQKNGIKVNFKIRHNIEDL
EQKLICISGDSLISLASTGKRVS IKDLLDEKDFEIWAVNEQTMKLESAKVS RVFCTGKKLVY
ILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLGLRGQYPYDVPDY
AIDZ

FIG._5R

CMV Promoter →

1 / 1	31 / 11	
GCT	TCG CGA TGT ACG GGC CAG ATA TAC GCG TTG ACA TTG ATT ATT GAC TAG TTA TTA ATA	
121 / 41	151 / 51	
TAC	GGT AAA TGG CCC GCC TGG CTG ACC GCC CAA CGA CCC CCG CCC ATT GAC GTC AAT AAT	
241 / 81	271 / 91	
TTT	ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA AGT GTA TCA TAT GCC AAG TAC GCC CCC	
361 / 121	391 / 131	
GGA	CTT TCC TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT GCG	
401 / 161	511 / 171	
CCA	CCC CAT TGA CGT CAA TGG GAG TTT GTT TTG GCA CCA AAA TCA ACG GGA CTT TCC AAA	
601 / 201	631 / 211	
CTA	TAT AAG CAG AGC TCT CTG GCT AAC TAG AGA ACC CAC TGC TTA CTG GCT TAT CGA AAT	
721 / 241	751 / 251	IntB (IC)
CTg	tcg act GGA GGA ACC	ATG GAG TCC GGA tca cca gaa ata gaa aag ttg tct cag agt
841 / 281	871 / 291	
ttg	act gtg cca gga cca cat aac ttt gtc gcc aat gac atc att gtc cat aac	agttATC
961 / 321	991 / 331	
ATG	ctc gag ggc caa gca ggt gga CTG ATC ACC acc agt	TGC ATC AGT GGA GAT AGt ttg
1081 / 361	1111 / 371	
ttt	gaa ata tgg gca att aat gaa cag acg atg atg aag cta gaa tca gct aaa gtt agt cgt	
1201 / 401	1231 / 411	
aag	gca aca aat cat aga ttt tta act att gat ggt tgg aaa aga tta gat gag cta	

FIG._6A

61 / 21	91 / 31	GTA ATC AAT TAC GGG GTC ATT AGT TCA TAG CCC ATA TAT GGA GTT CCG CGT TAC ATA ACT
181 / 61	211 / 71	GAC GTA TGT TCC CAT AGT AAC GCC AAT AGG GAC TTT CCA TTG ACG TCA ATG GGT GGA CTA
301 / 101	331 / 111	TAT TGA CGT CAA TGA CGG TAA ATG GCC CGC CTG GCA TTA TGC CCA GTA CAT GAC CTT ATC
421 / 141	451 / 151	GTT TTG GCA GTA CAT CAA TGG GCG TGG ATA GCG GTT TGA CTC ACG GGG ATT TCC AAG TCT
541 / 181	571 / 191	ATG TCG TAA CAA CTC CGC CCC ATT GAC GCA AAT GGG CGG TAG GCG TGT ACG GTG GGA GGT
661 / 221	691 / 231	TAA TAC GAC TCA CTA TAG GGA GAC CCA AGC TGG CTA GTT AAG CTT cct ata cta gga GAT
781 / 261	811 / 271	gat att tac tgg gac tcc atc atc gtt tct att acg gag act gga gtc gaa gag gtt ttt gat
901 / 301	931 / 311	Flag Epitope Insert
1021 / 341	1051 / 351	GAA CAA ggc cag ggc ggt ggc ATG TCA ATG gac tat aaa gat gac gat aag ATG AGG
1141 / 381	1171 / 391	IntA (IN)
1261 / 421	1291 / 431	tct tta aaa gag cat att gct cta ccc cgt aaa cta gaa agc tcc tct tta caa tta ATC

FIG..6B

+

GAT D	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	L
M	V	S	K	G	E	E	L	F	T	G	V	V	P	I	L	V	E			
TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	P
Y	G	K	L	T	L	K	F	I	C	T	T	G	K	L	P	V	P	W	P	
AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	
K	Q	H	D	F	F	K	S	A	M	P	E	G	Y	V	Q	E	R	T	I	
CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	
L	V	N	R	I	E	L	K	G	I	D	F	K	E	D	G	N	I	L	G	
AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	CAG	CTC	
N	G	I	K	V	N	F	K	I	R	H	N	I	E	D	G	S	V	Q	L	
CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	
H	Y	L	S	T	Q	S	A	L	S	K	D	P	N	E	K	R	D	H	M	

TAA
*

FIG._6C

+

GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAT	GCC	ACC
D	G	D	V	N	G	H	K	F	S	V	S	G	E	G	D	A	T
GFP																	
ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC
T	L	V	T	T	L	T	Y	G	V	Q	C	F	S	R	Y	P	D
GFP																	
TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC
F	K	D	D	N	G	N	Y	K	T	R	A	E	V	K	F	G	D
GFP																	
CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	AAG	CAG
H	K	L	E	Y	N	Y	N	S	H	N	V	Y	I	M	A	D	K
GFP																	
GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	CCC	GTG	CTG	CCC	GAC
A	D	H	Y	Q	Q	N	T	P	I	G	D	G	P	V	L	P	D
GFP																	
GTC	CTG	CTG	GAG	TTC	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	CTG	TAC
V	L	L	E	F	V	T	A	A	G	I	T	L	G	M	D	E	Y

FIG._6D

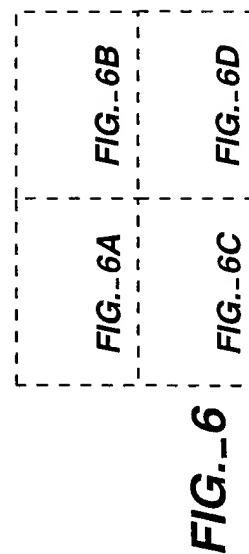


FIG._6

+

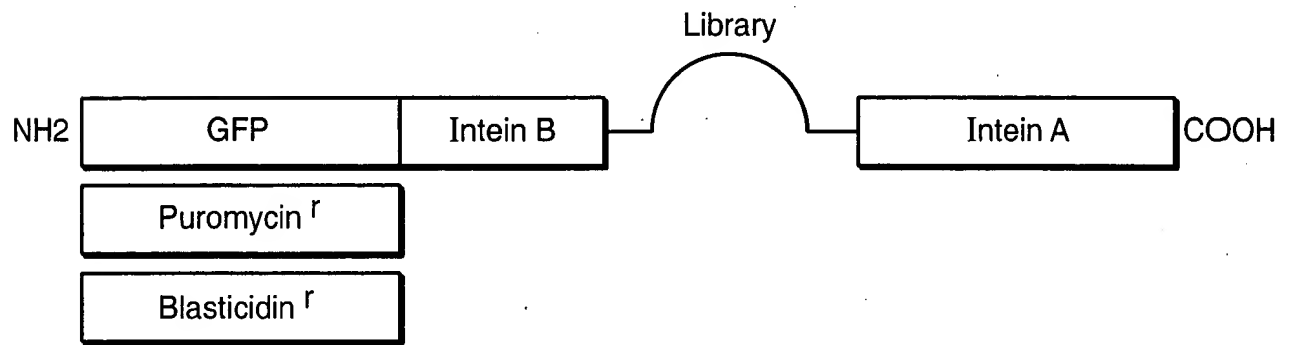
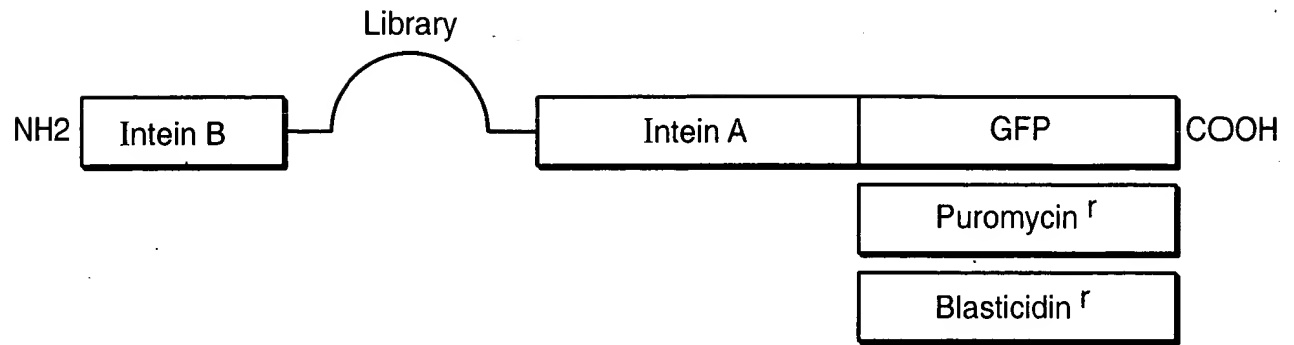
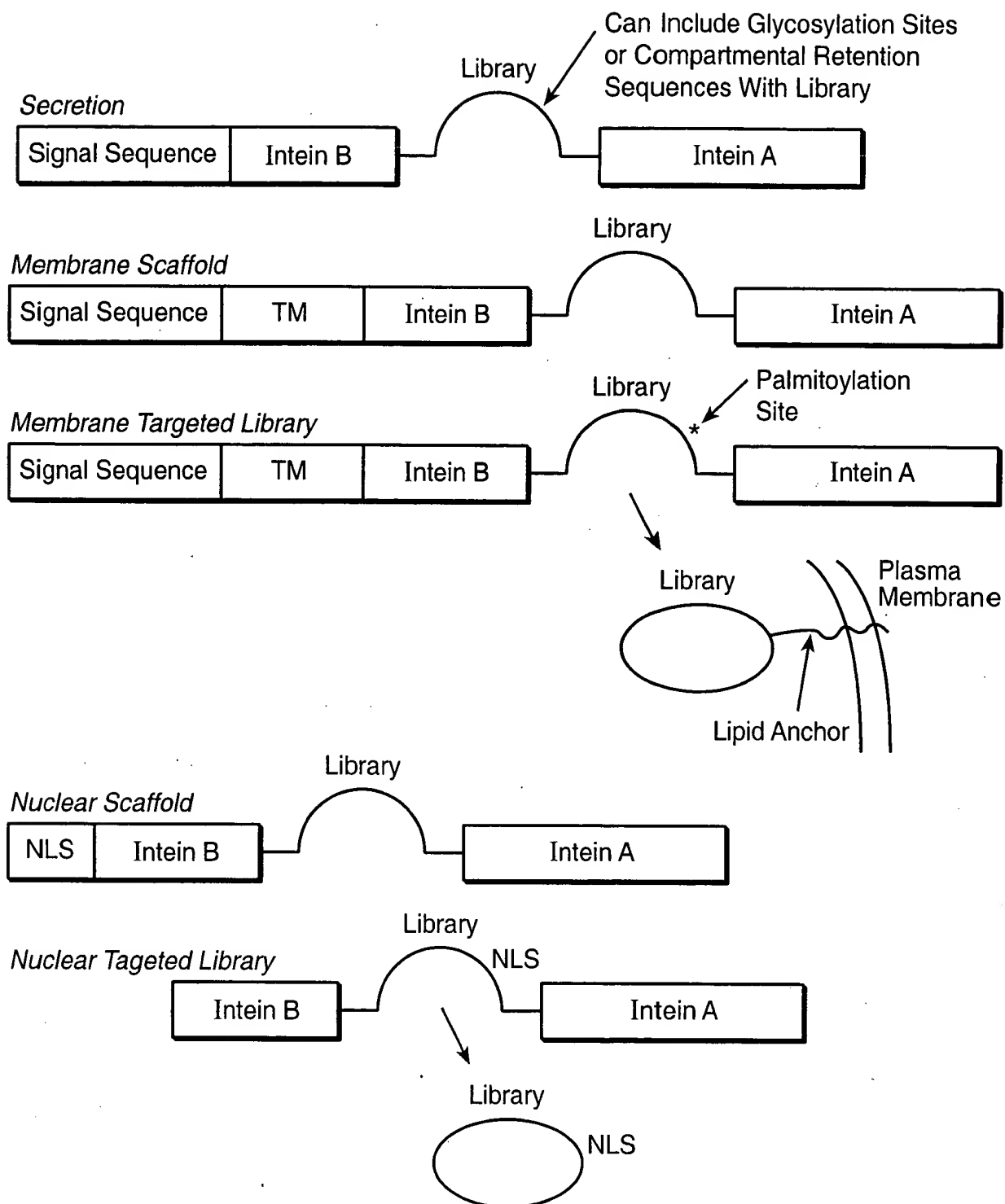
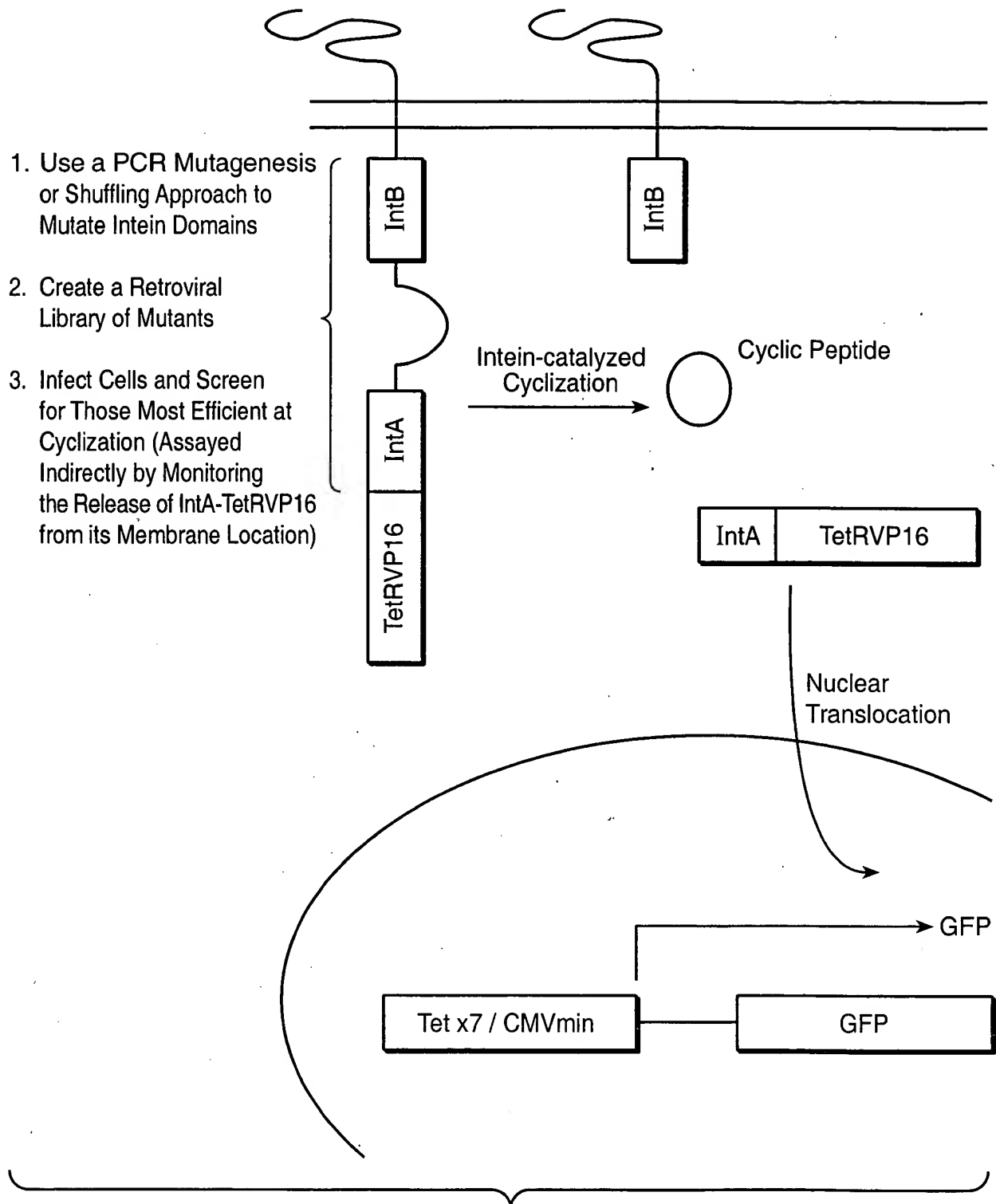


FIG. 7

**FIG._8**

**FIG._9**

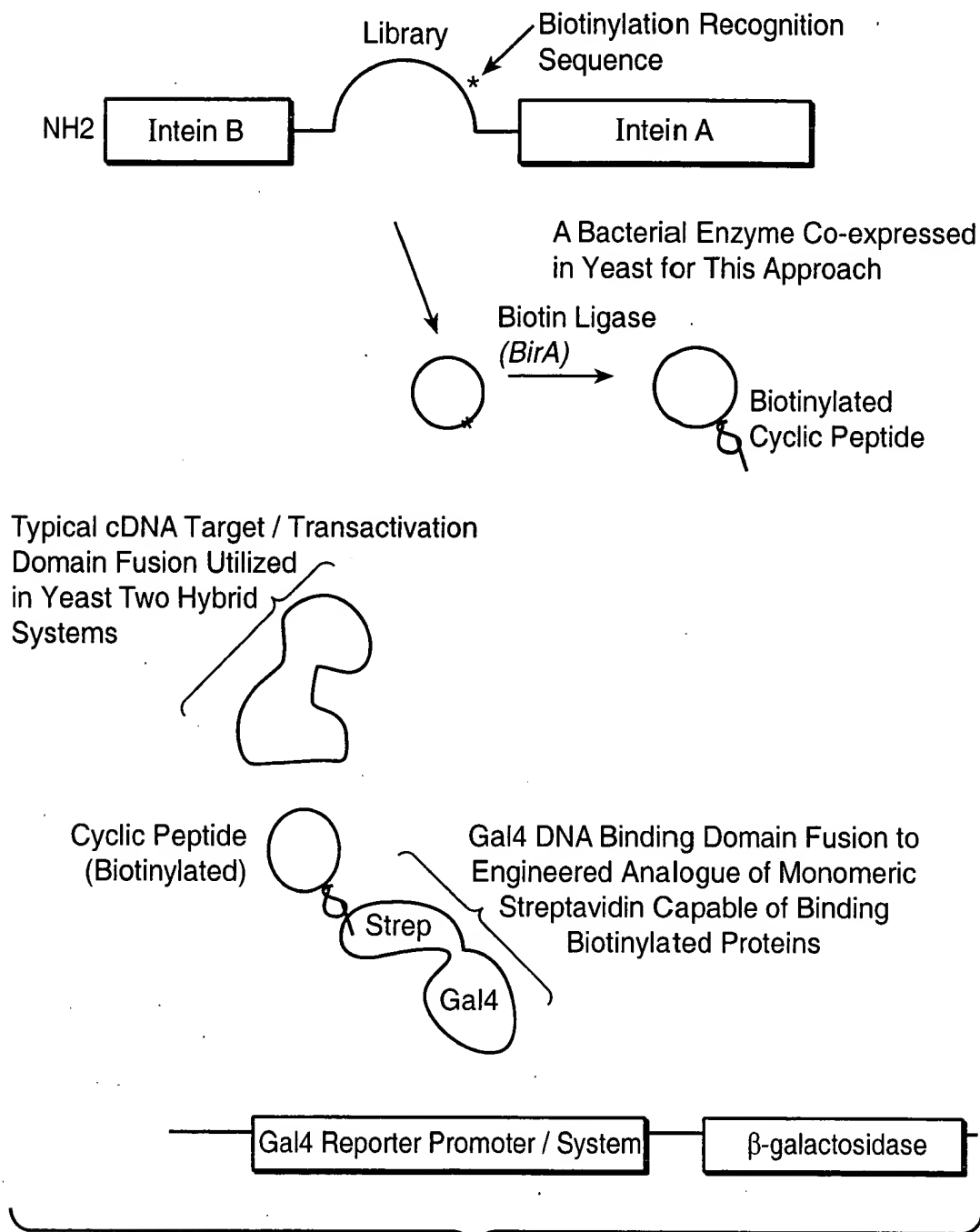


FIG. 10

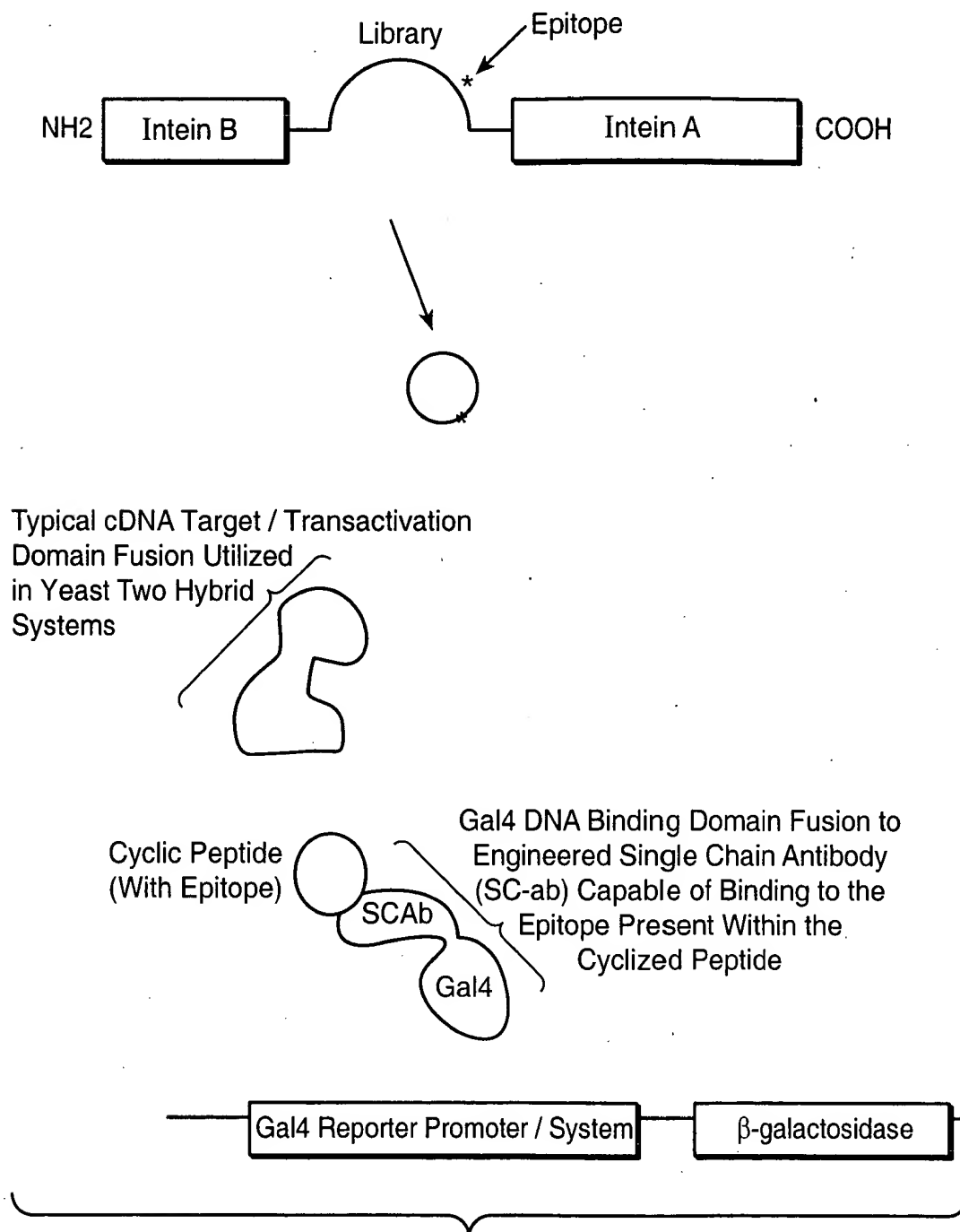


FIG. 11

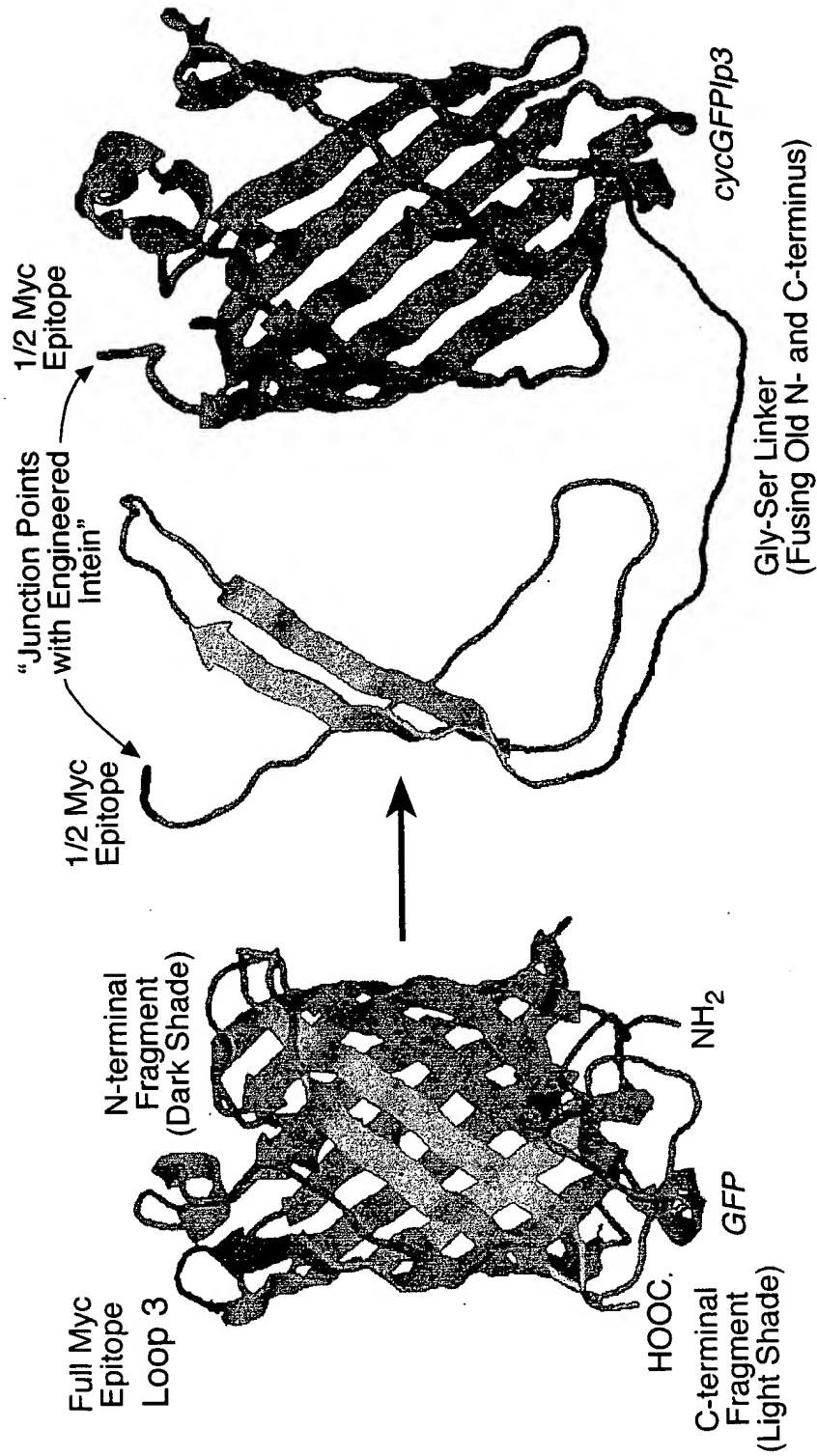


FIG. 12A

IntB (Ic)

MESGSPETIEKLSQSDIYWDSIVSITETGVVEEVFDLTVPGP

myc⁶⁻¹⁰

HNFVANDIIVHNSEEDLGSSVQLADHYQQNTPIGDGPVLL

PDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITLGMDE

Gly-Ser Linker

LYKGSNGEFSQVDKSMVSKGEELFTGVVPILVELDGDVNG

GFP⁶⁻¹⁻¹⁷³

HKFSVSGEGEGDATYGLKTLKFICTTGKLPVPWPTLVTTL

TYGLQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDG

NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN

myc¹⁻⁵

YNSHNVYIMADKQKNGIKVNFKIRHNIEDLEQKLIICISGD

SLISLASTGKRVSISKDLLDEKDFEIWAINETMKLES AKV

IntA (IN)

SRVFCTGKKLVYILKTRLGRTIKATANHRELTIDGWKRDL

HA

ELSKLEHIALPRKLESSSLQLGLRGQYPYDVPDYAID

FIG._12B

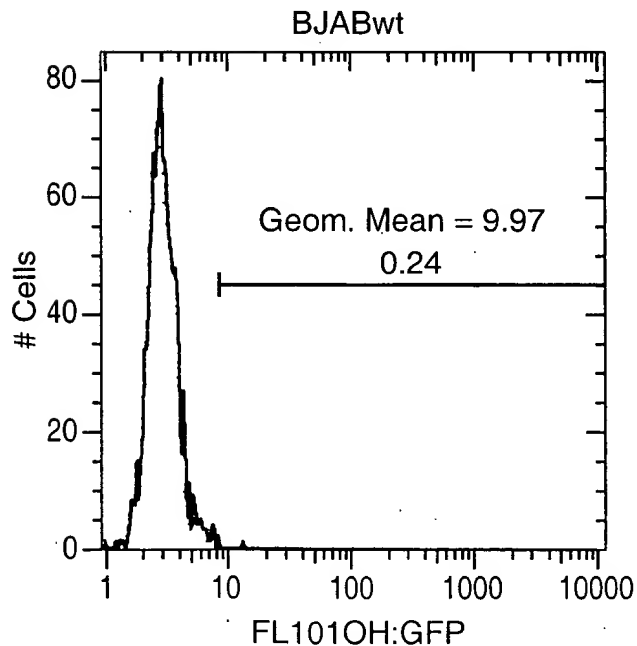


FIG._12D-1

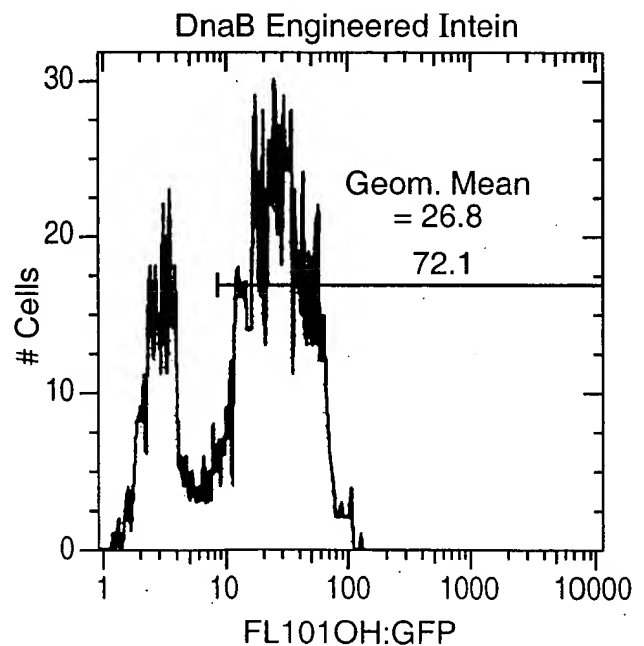


FIG._12D-2

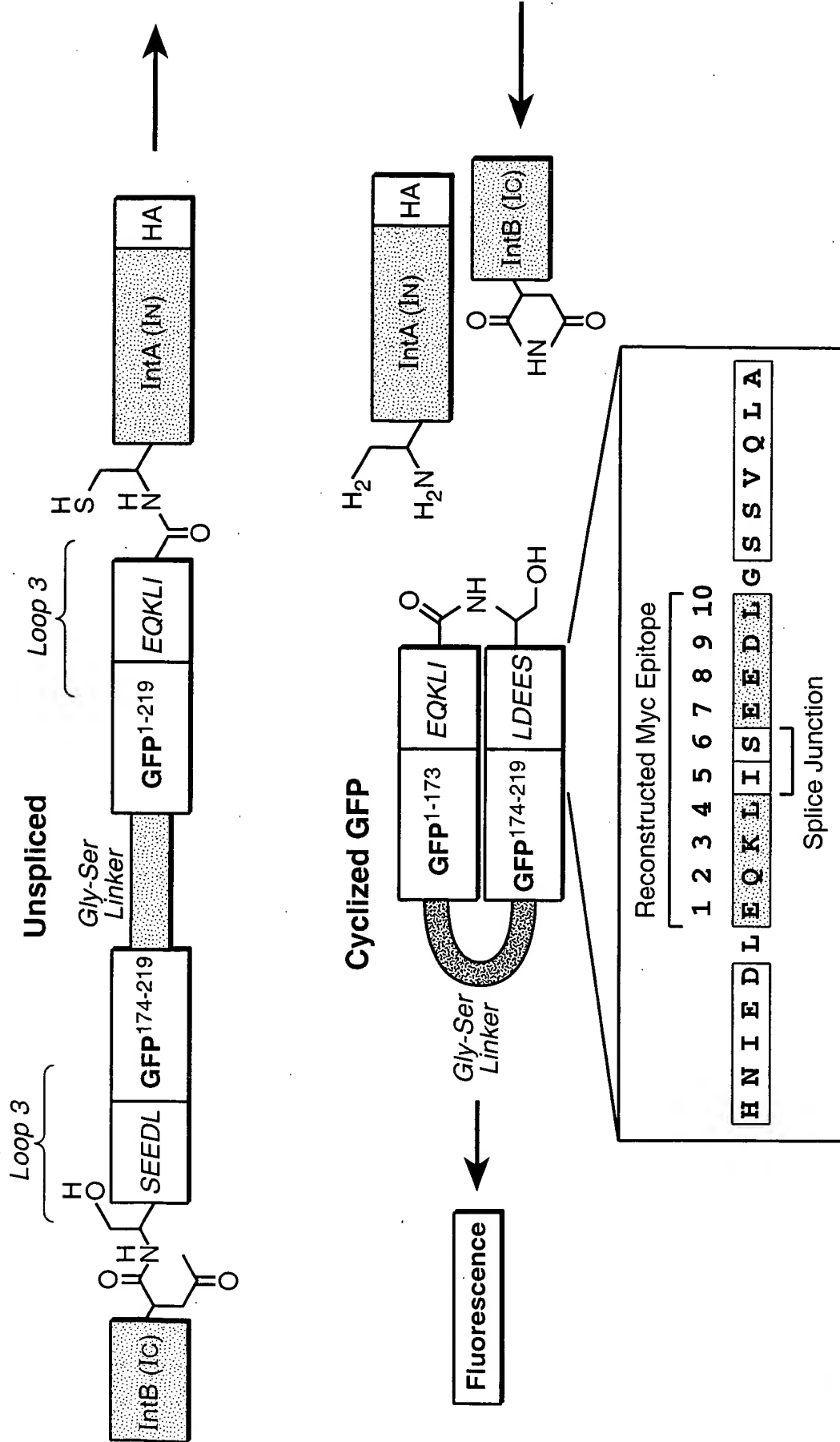
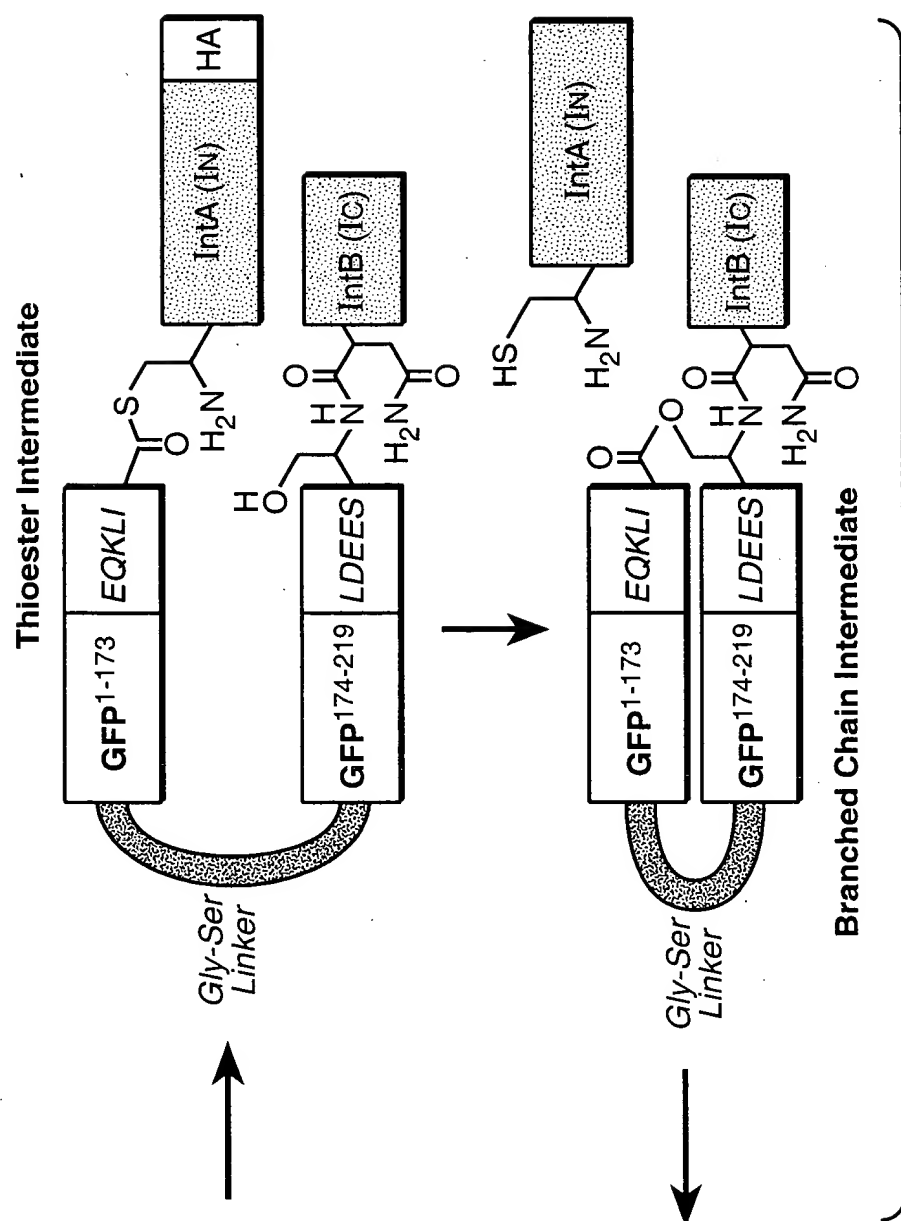


FIG._12C-1



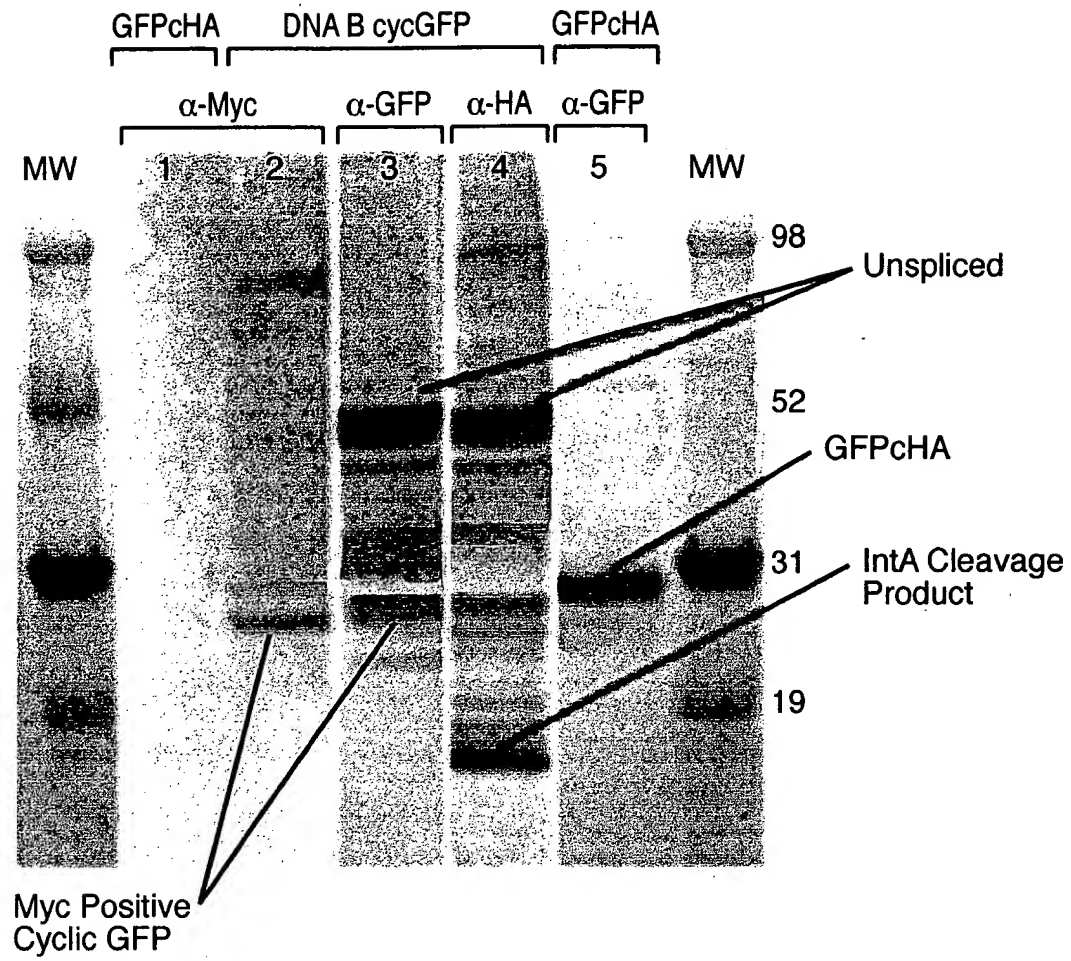


FIG._12E

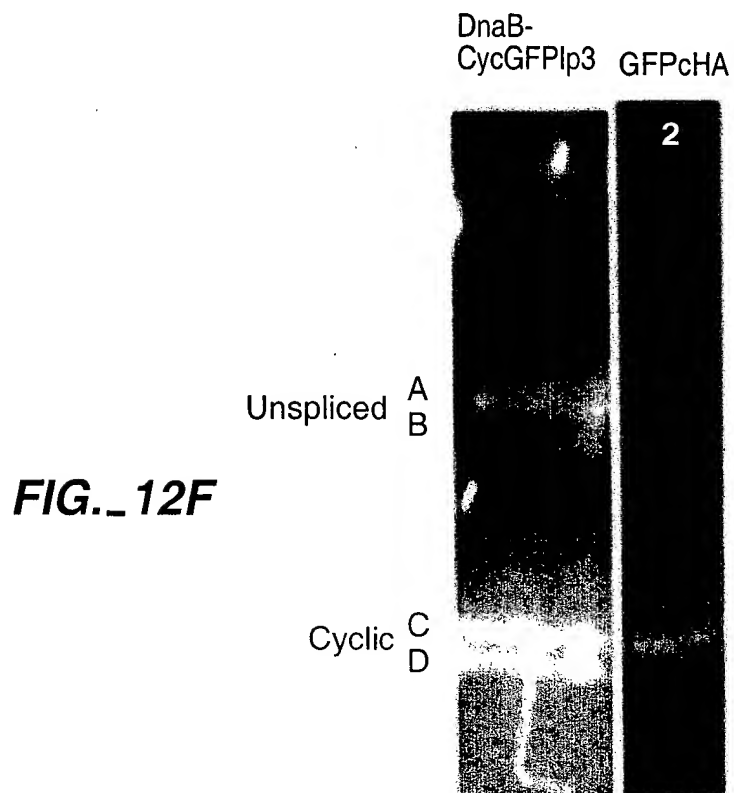
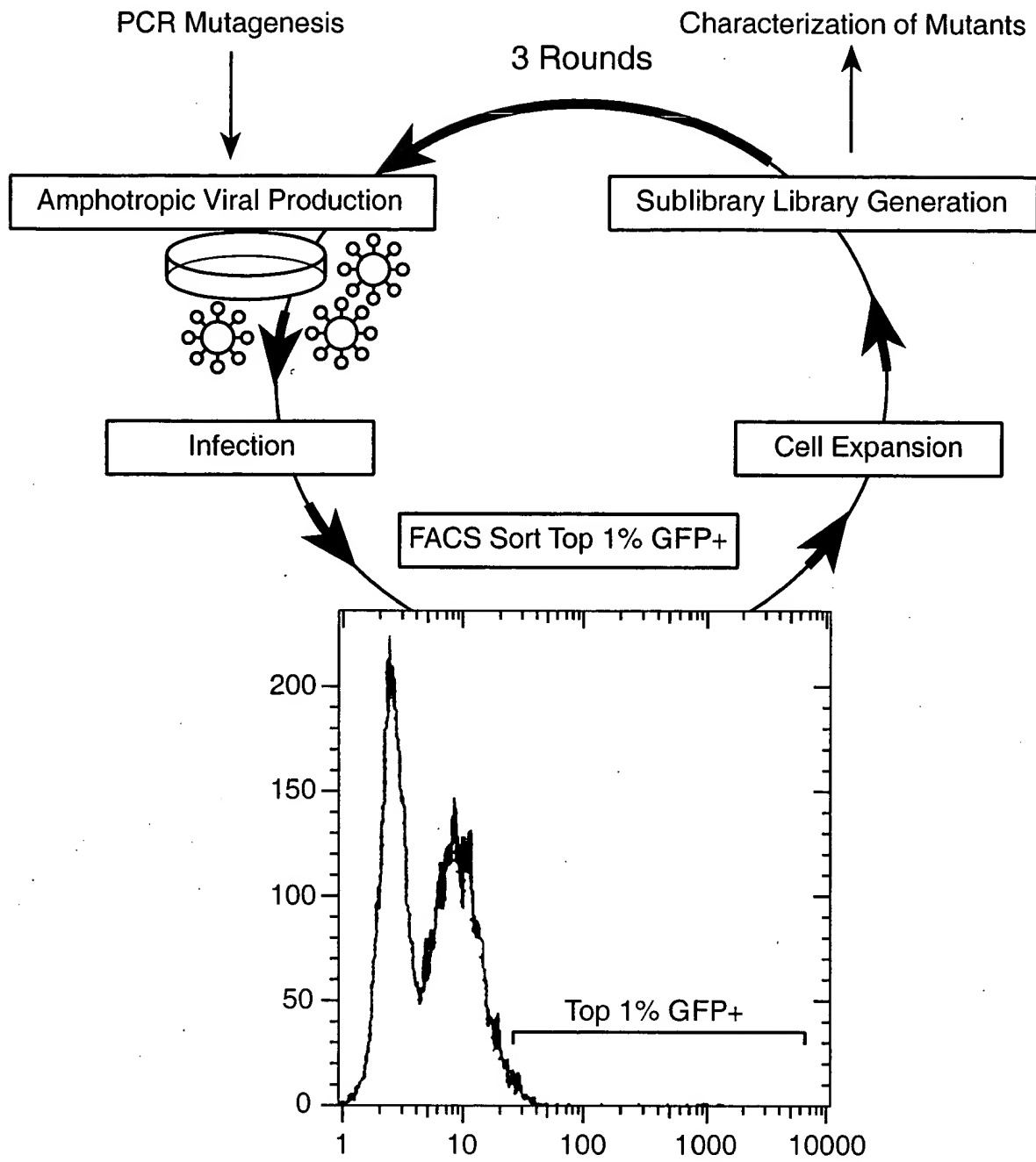


FIG._12F

**FIG. 13A**

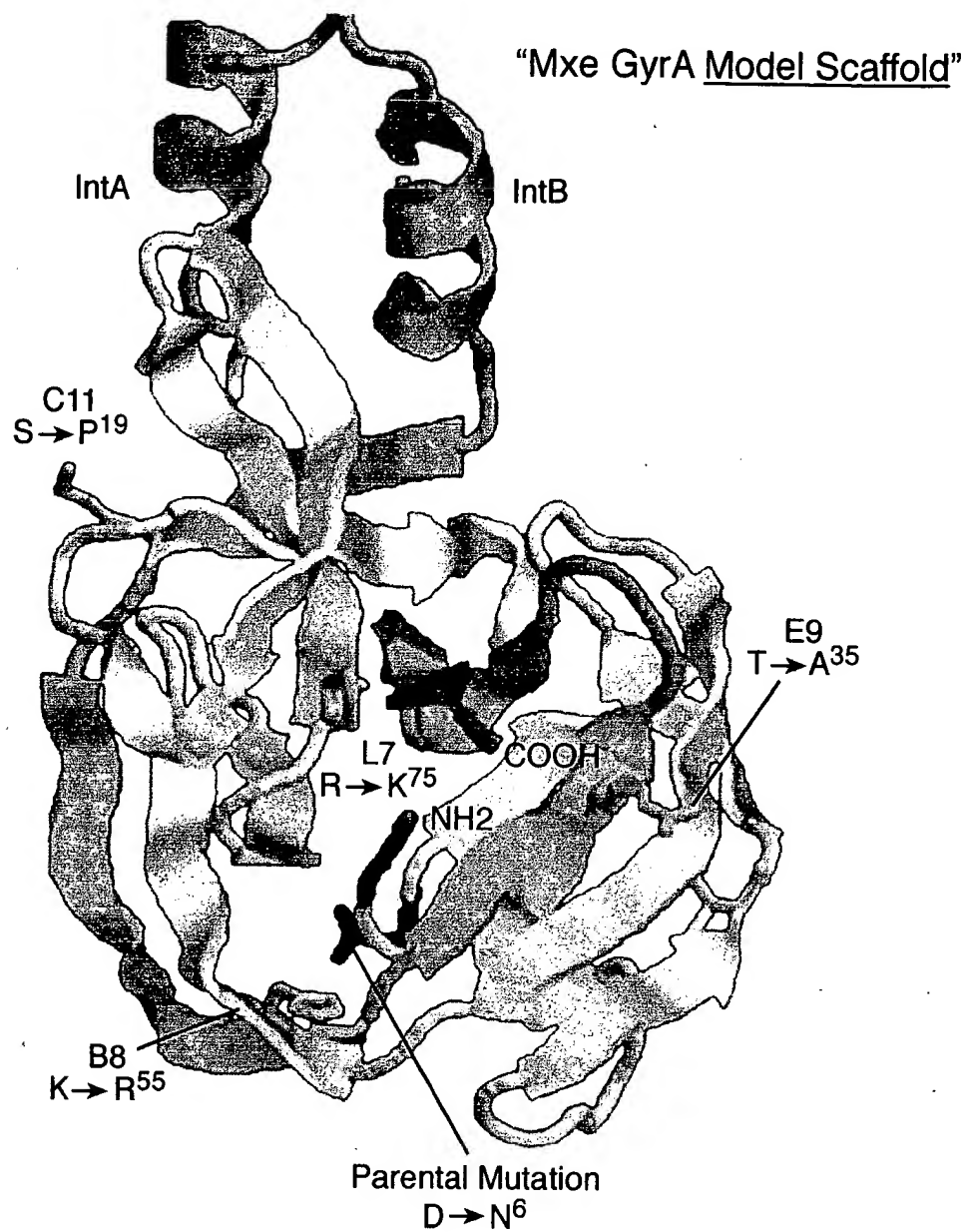


FIG. 13B

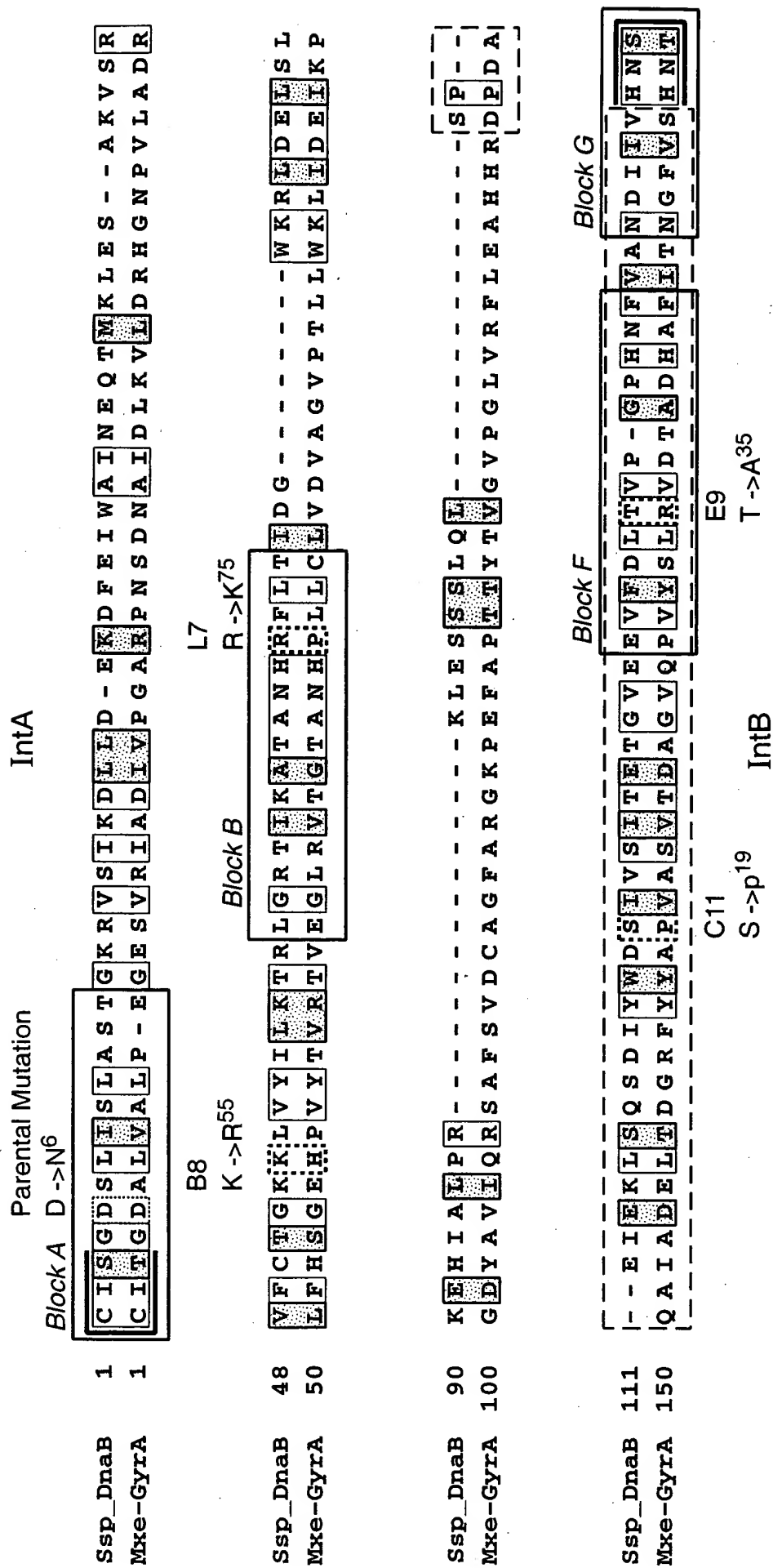
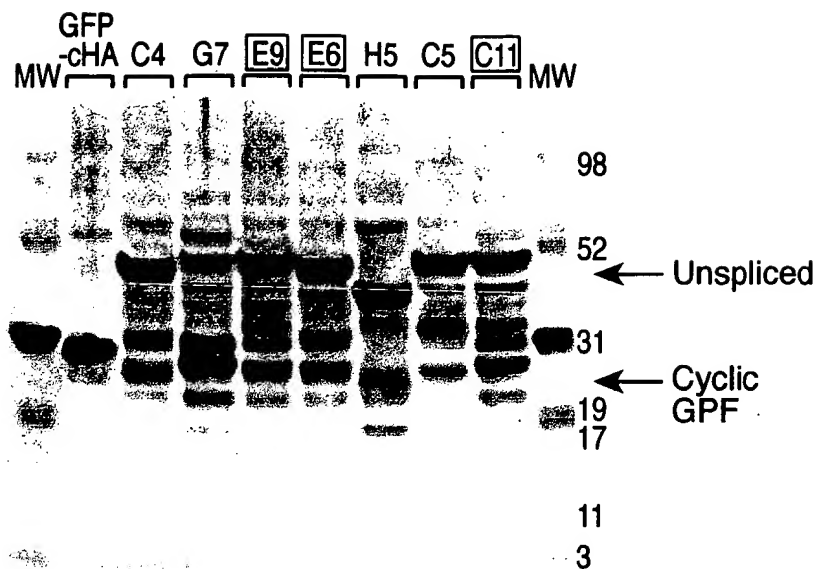
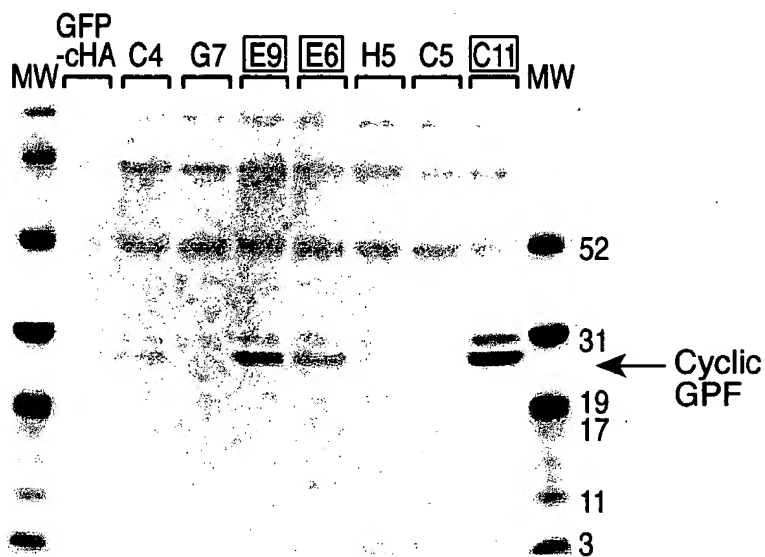


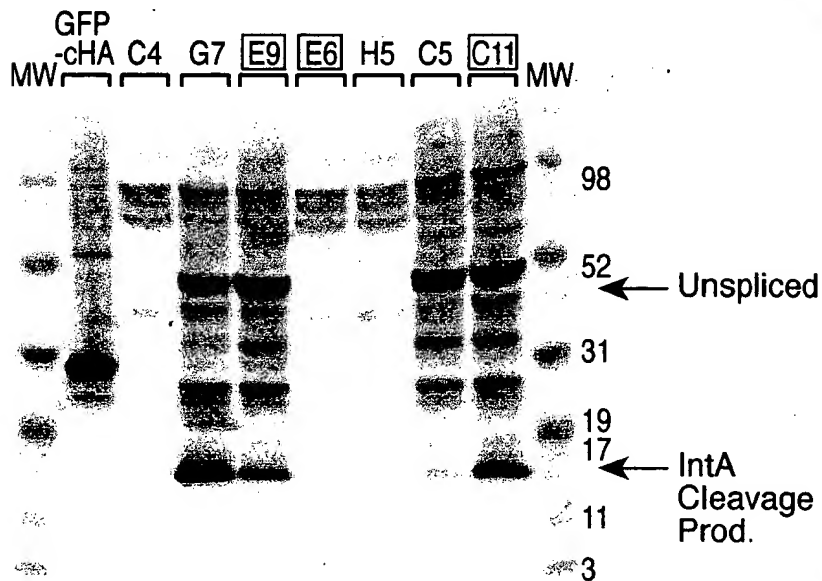
FIG. 13C

**FIG. 13D-1**

α-GFP
Identifies All Splice Intermediates and Final Product

**FIG. 13D-2**

α-myc
Identifies Only Cyclic Product with Reconstructed Myc Epitope

**FIG. 13D-3**

α-Flu
Identifies IntA Splice Intermediates and Cleavage Product

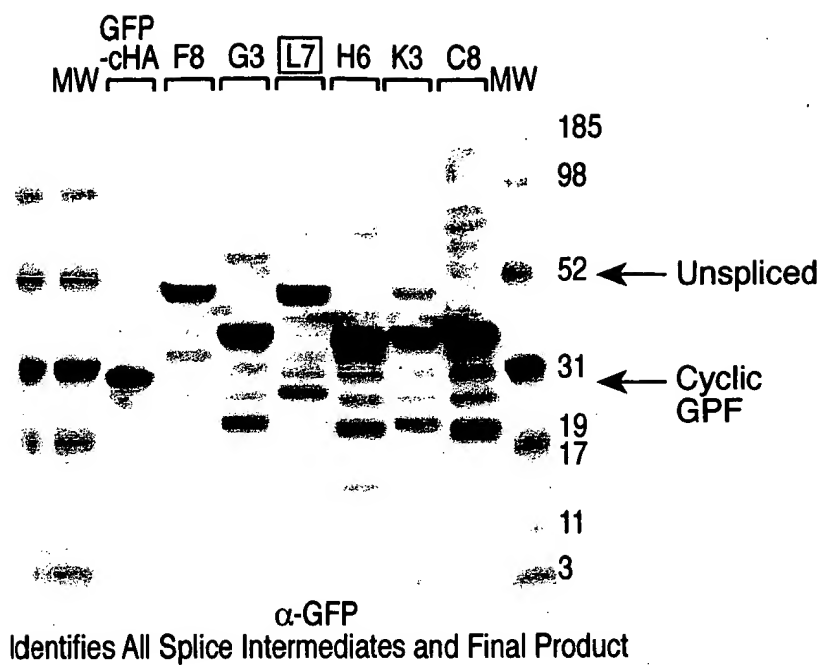


FIG._13D-4

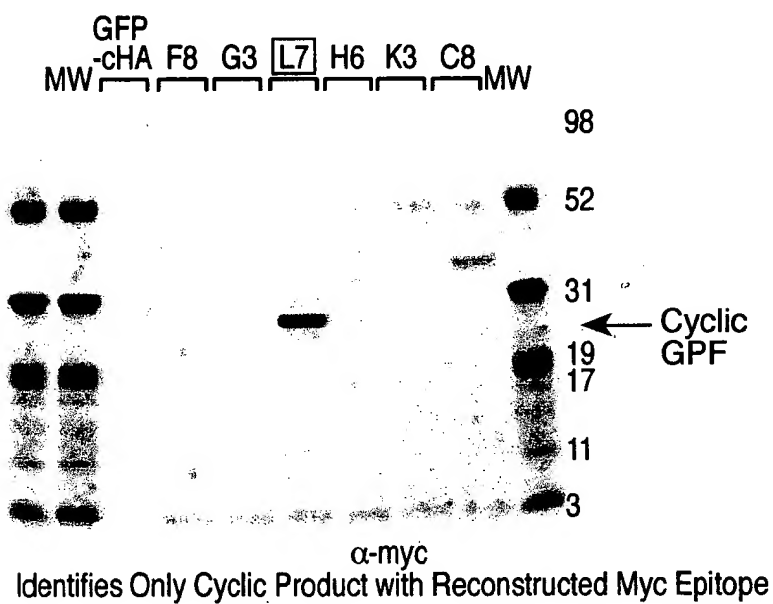


FIG._13D-5

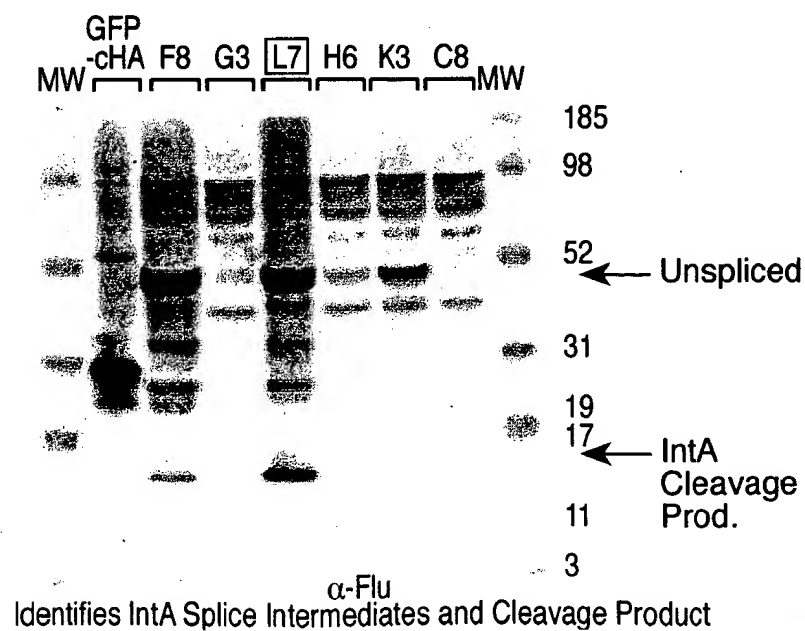


FIG._13D-6

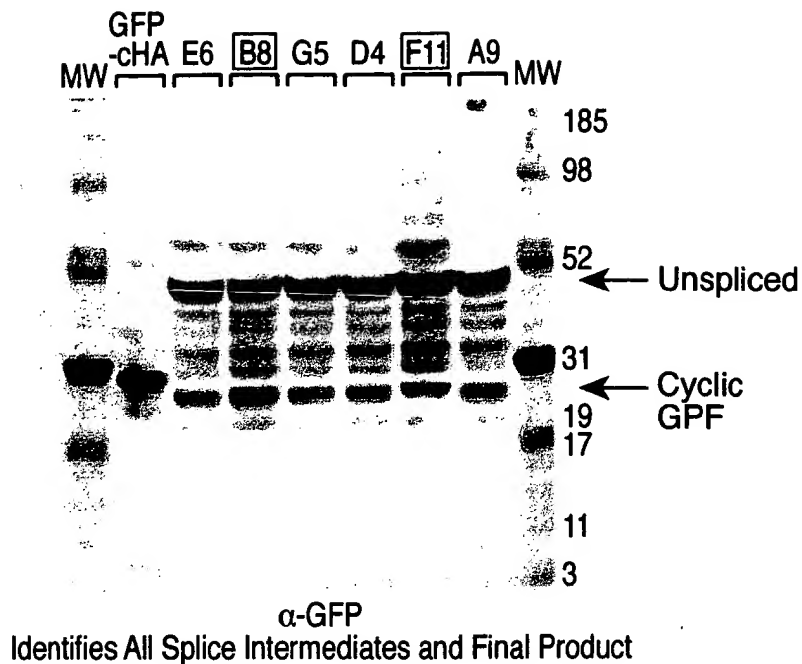


FIG._13D-7

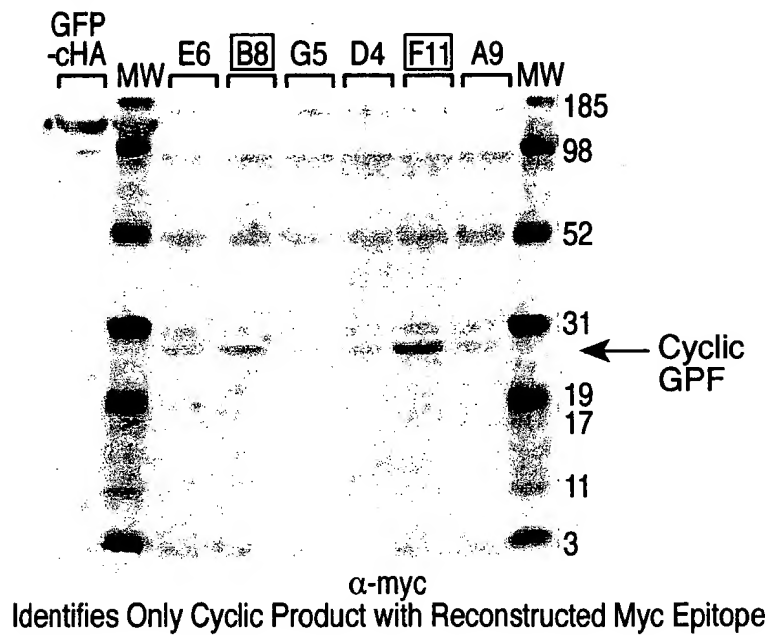


FIG._13D-8

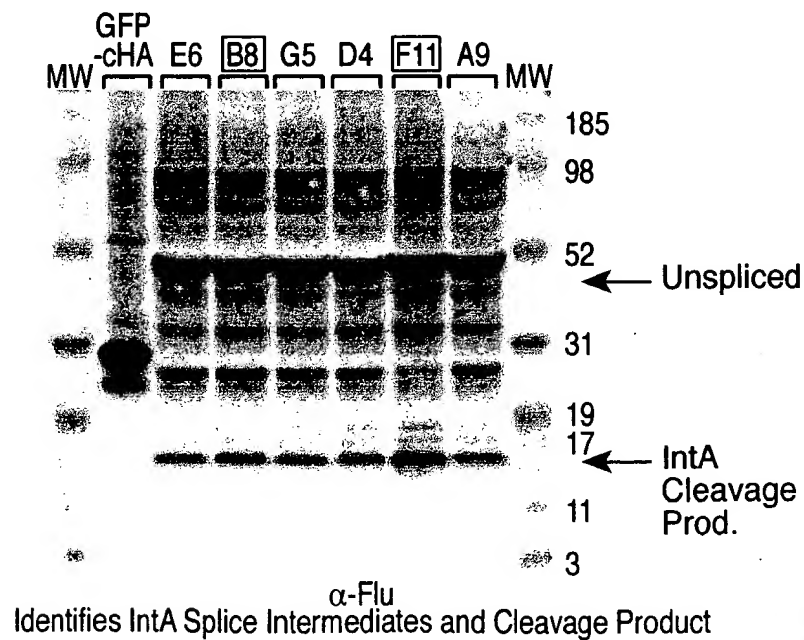


FIG._13D-9

+

Transfected PhxA Cells

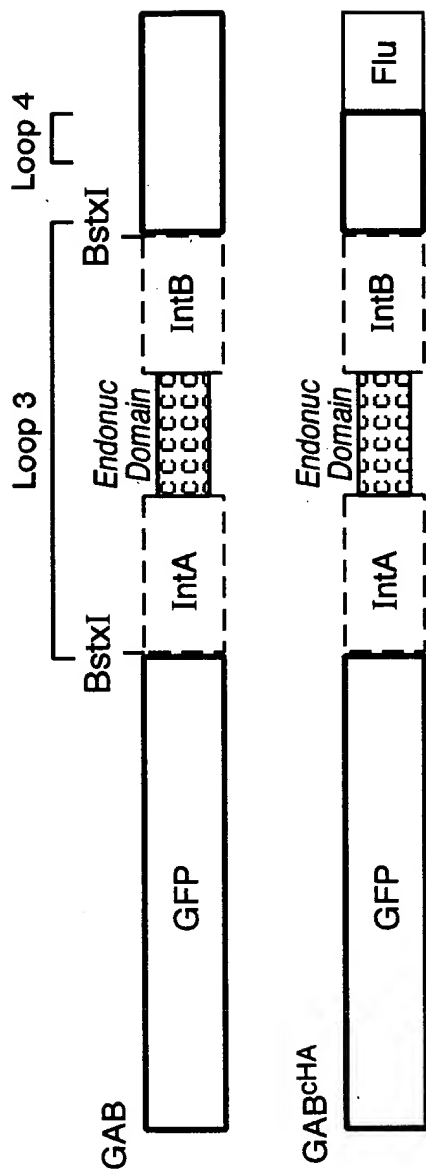
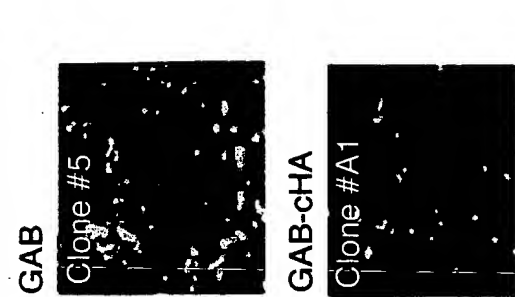


FIG. 14A

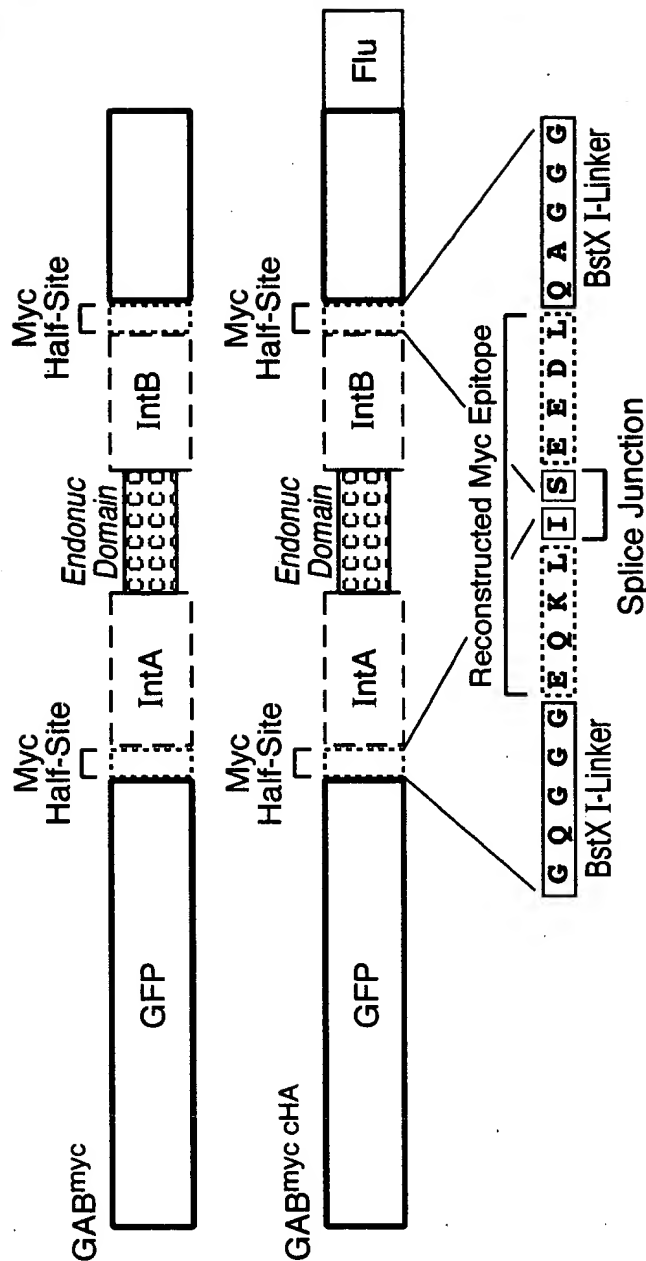
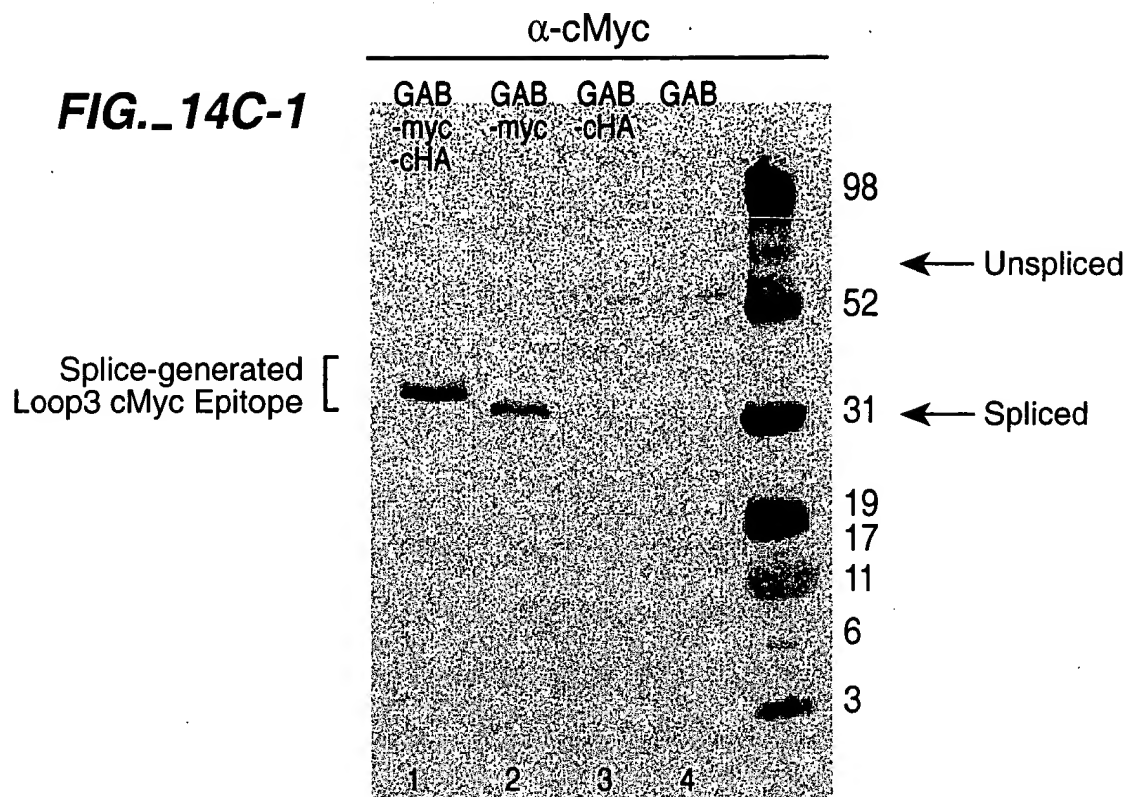
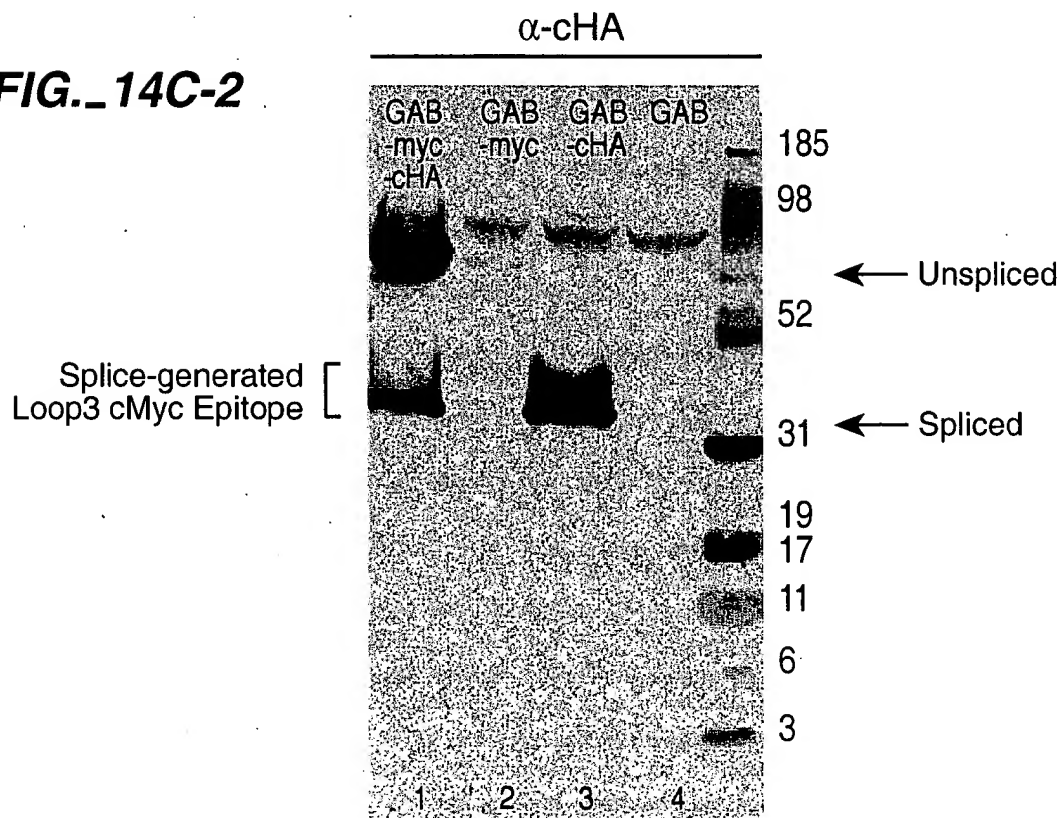
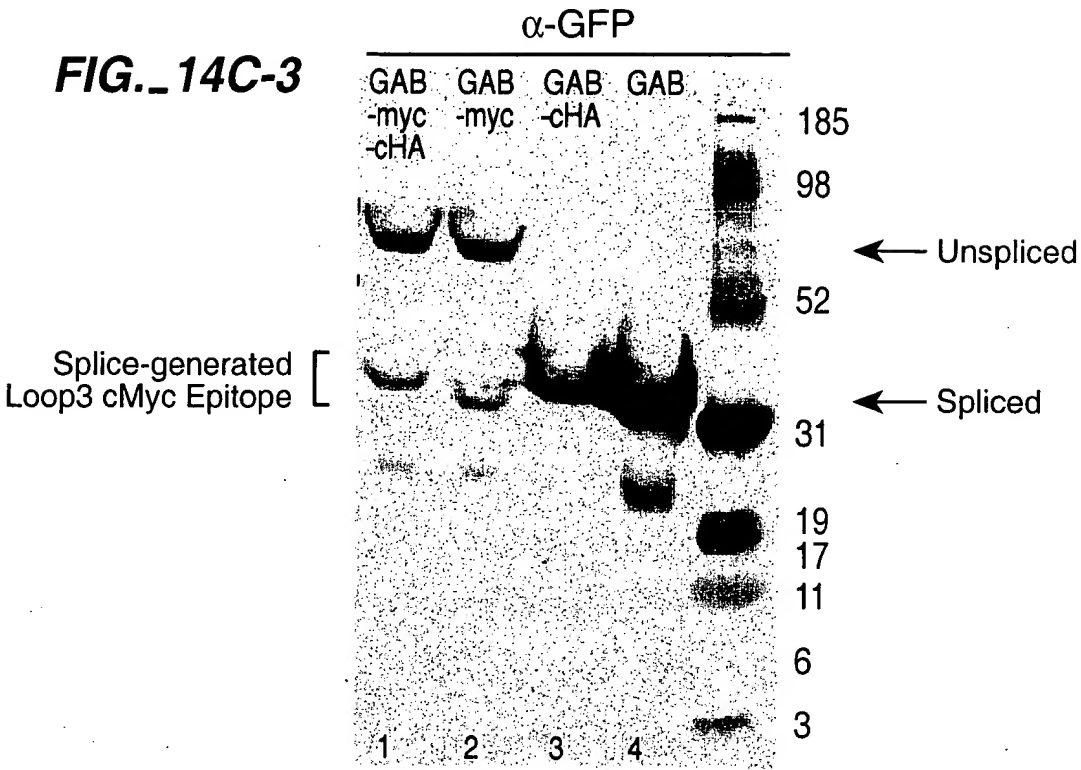


FIG. 14B

FIG._14C-1**FIG._14C-2**



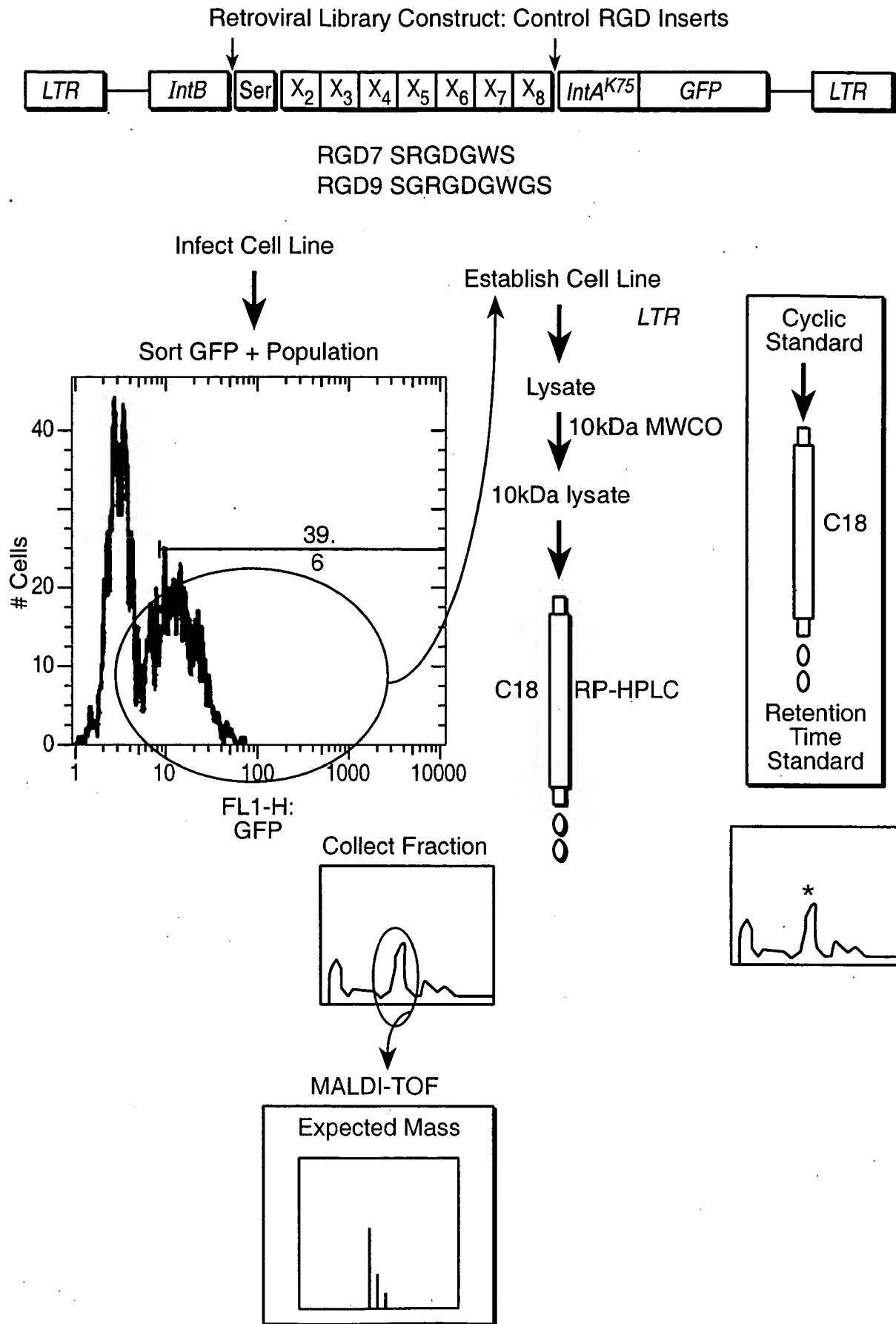


FIG. 15A

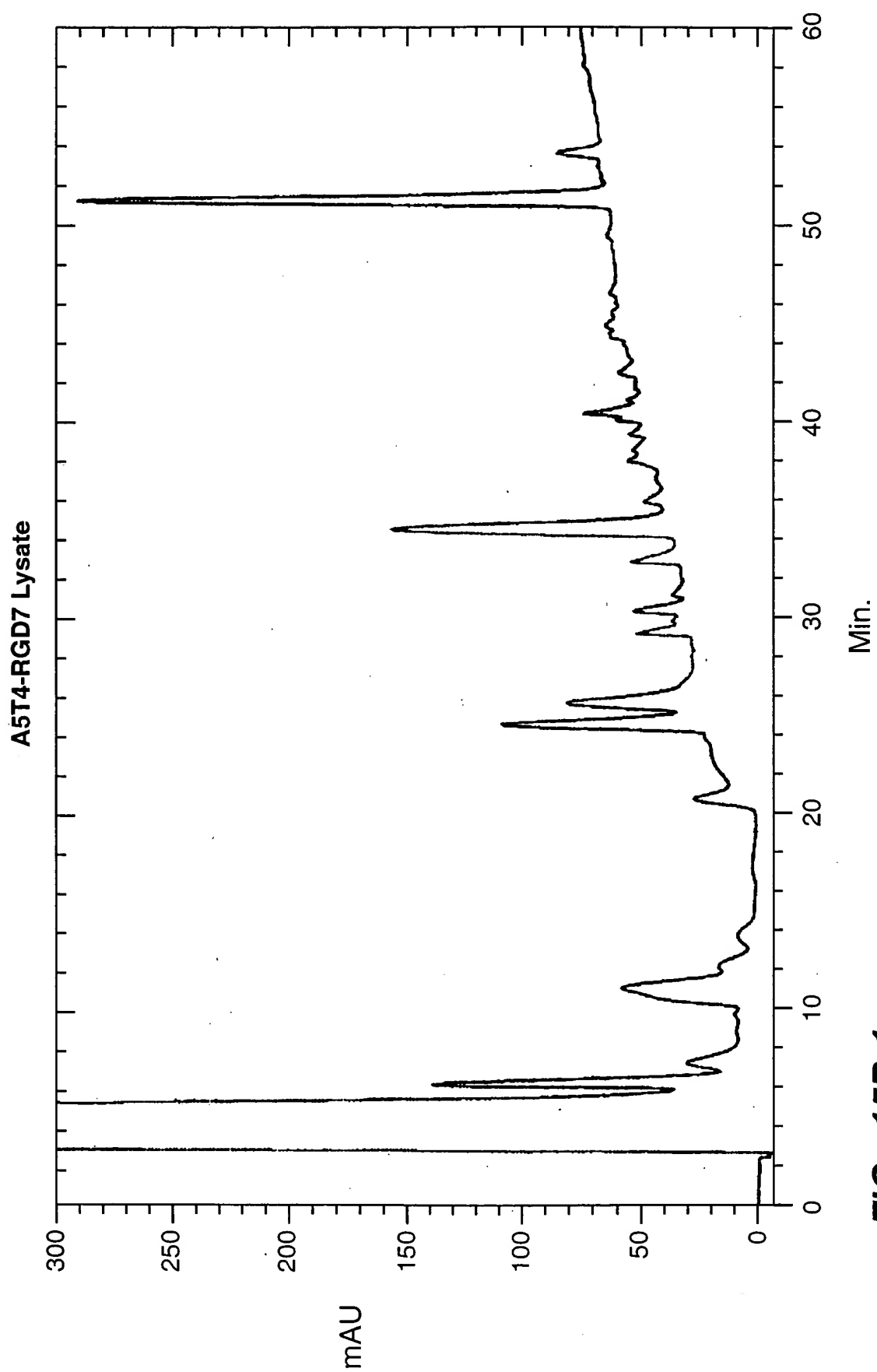
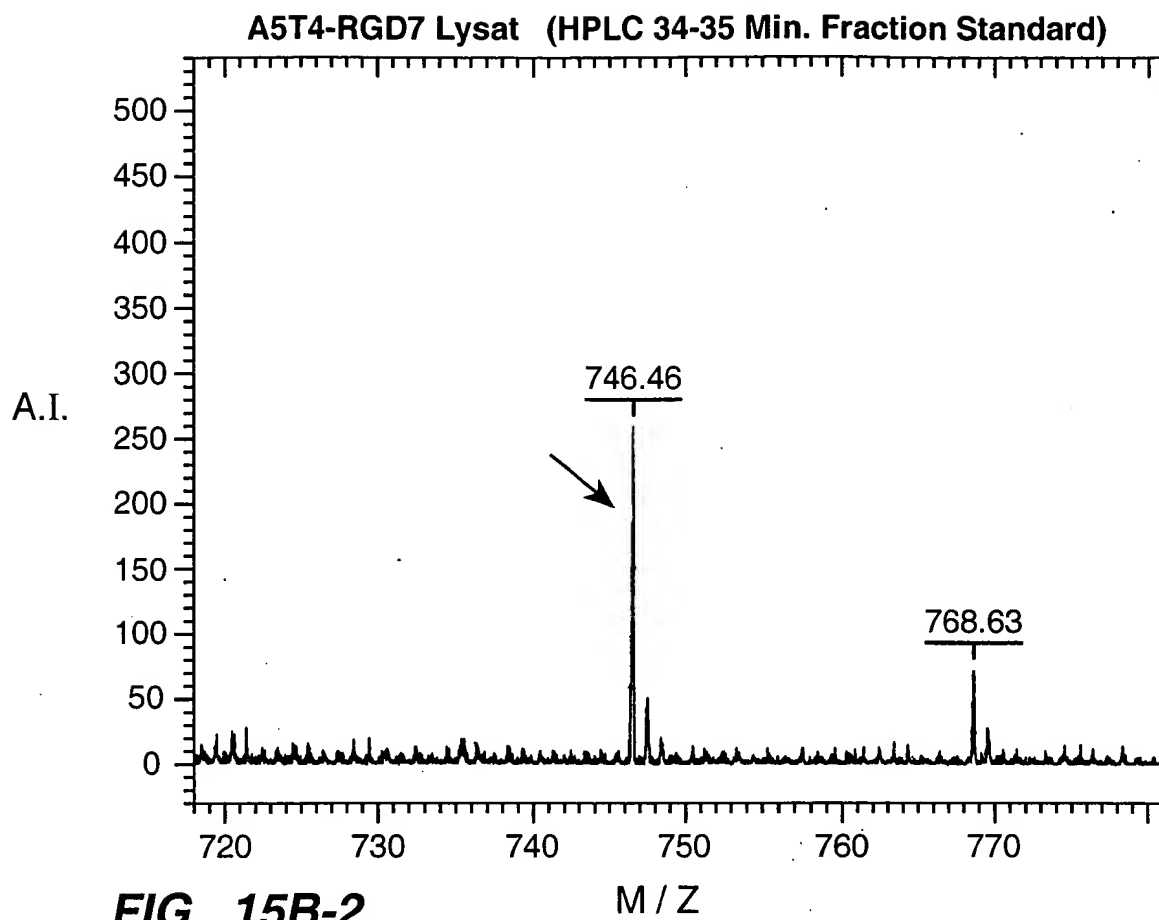
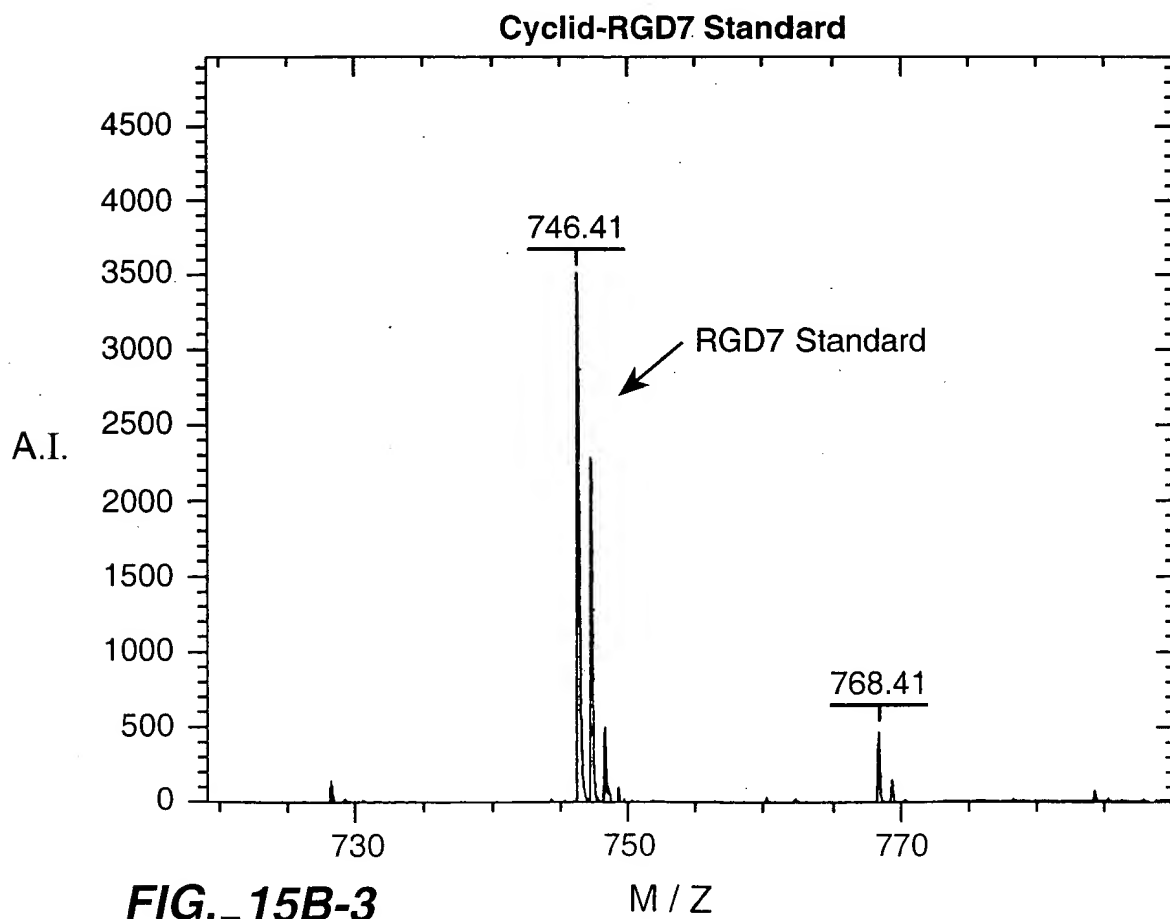
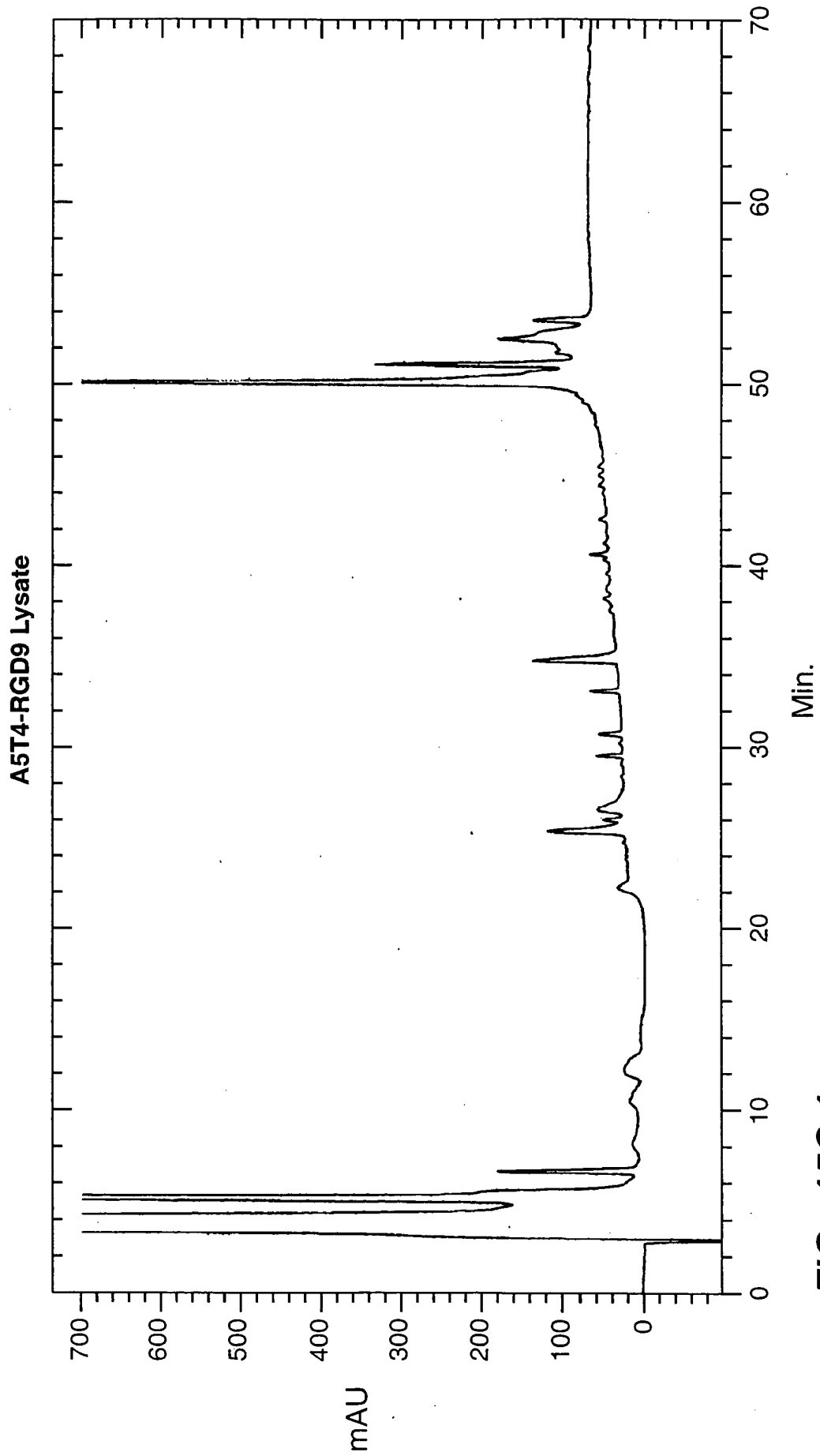


FIG._15B-1

**FIG._15B-2****FIG._15B-3**

**FIG._15C-1**

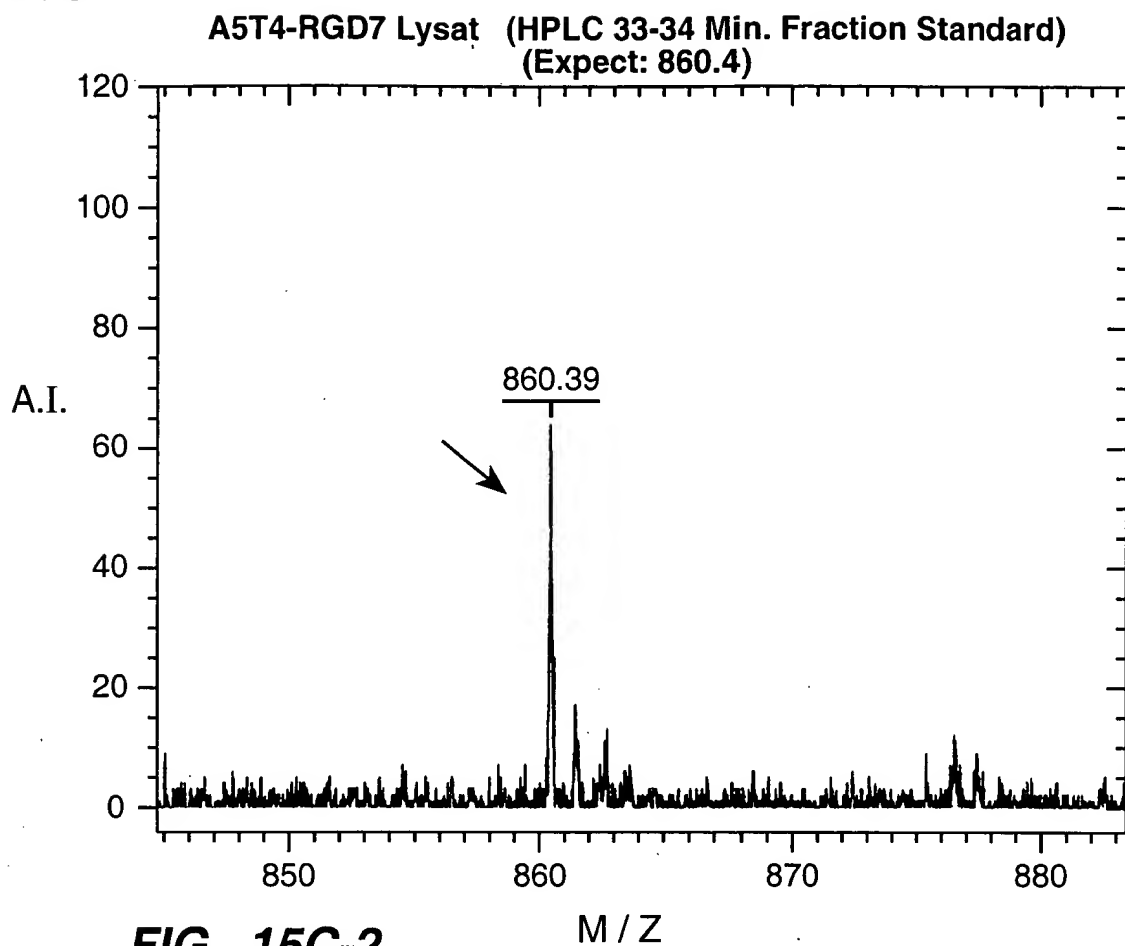


FIG._15C-2

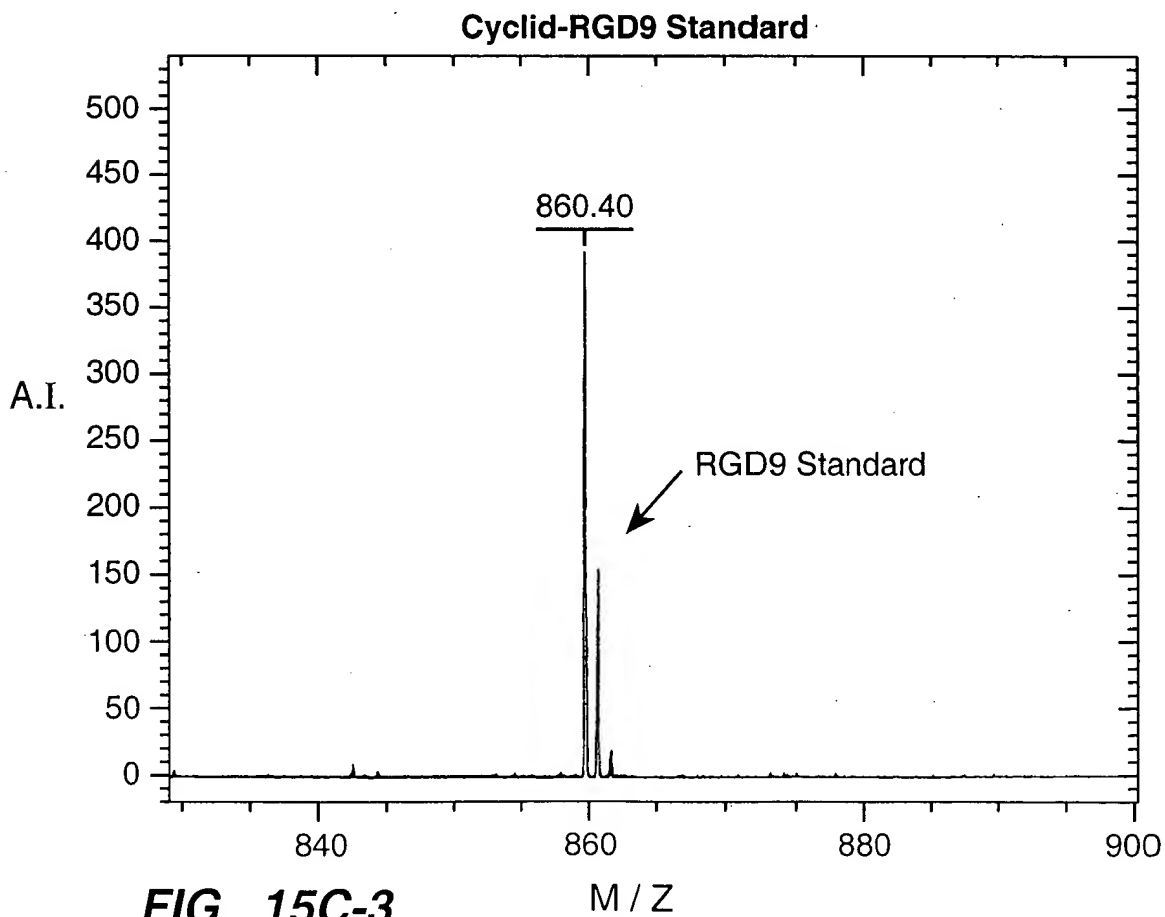


FIG._15C-3

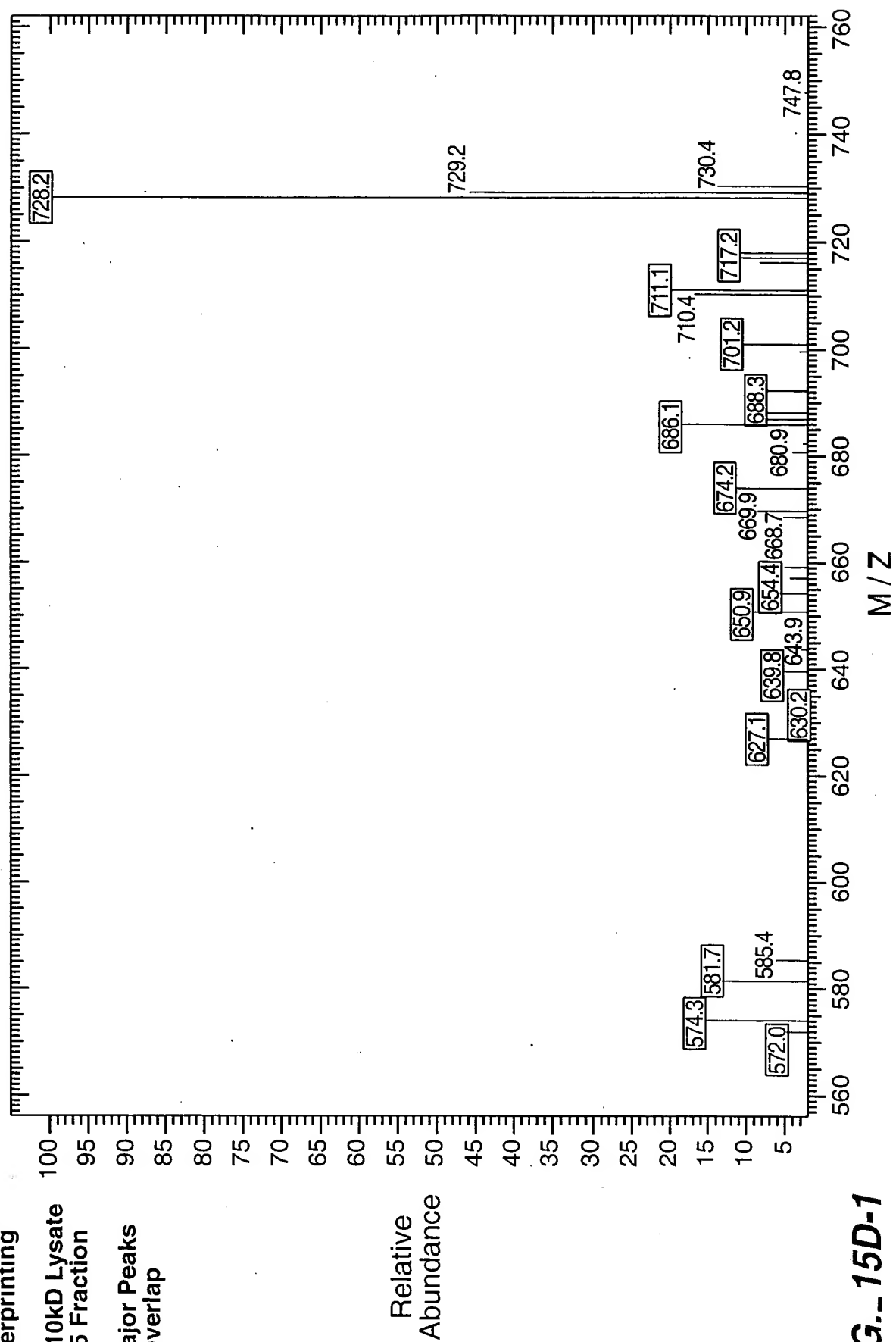
LC / MS Fragmentation
FingerprintingRGD7 10kD Lysate
34-35 Fraction15 Major Peaks
Overlap

FIG..15D-1

RGD7 Standard

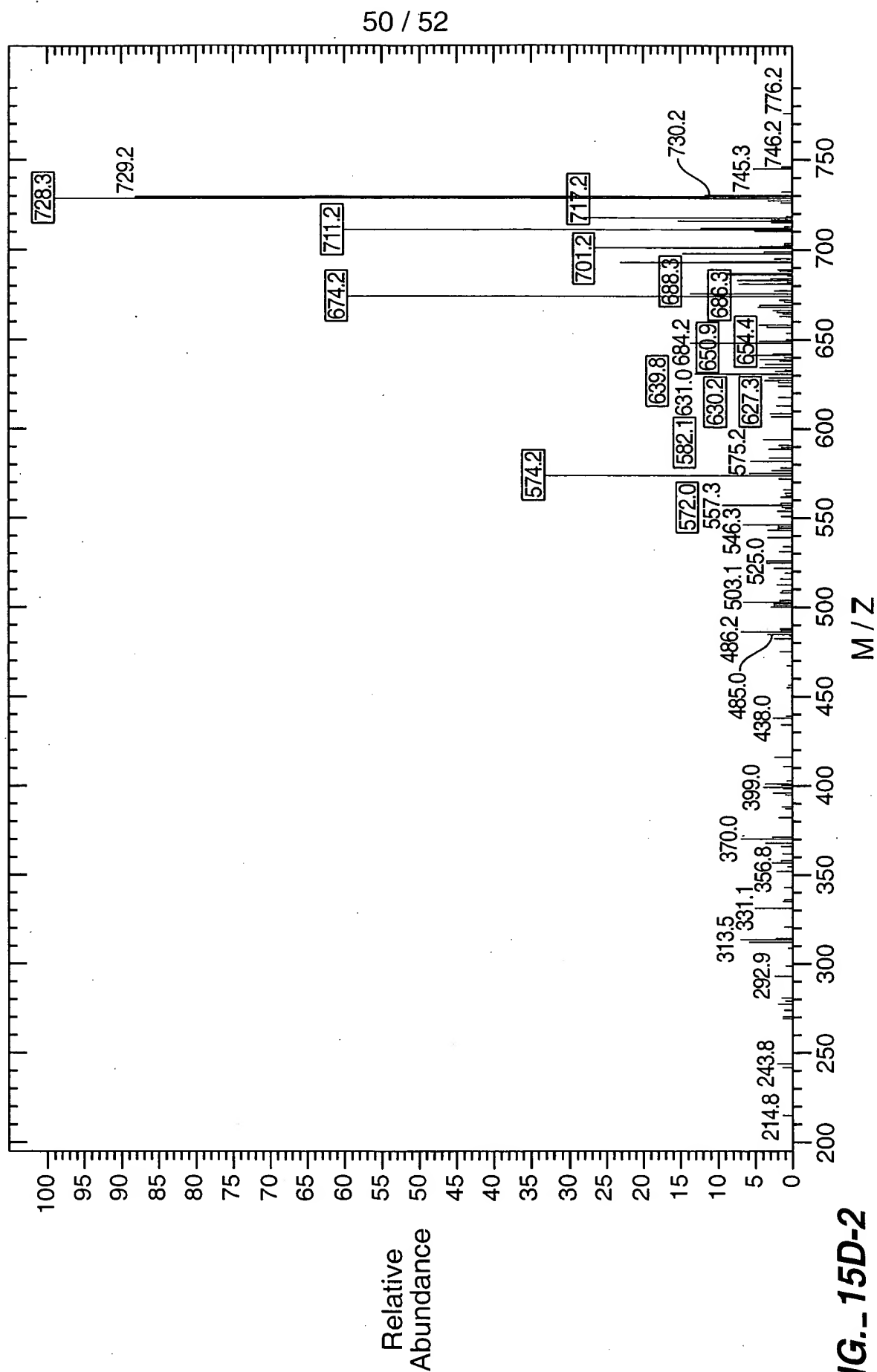


FIG..15D-2

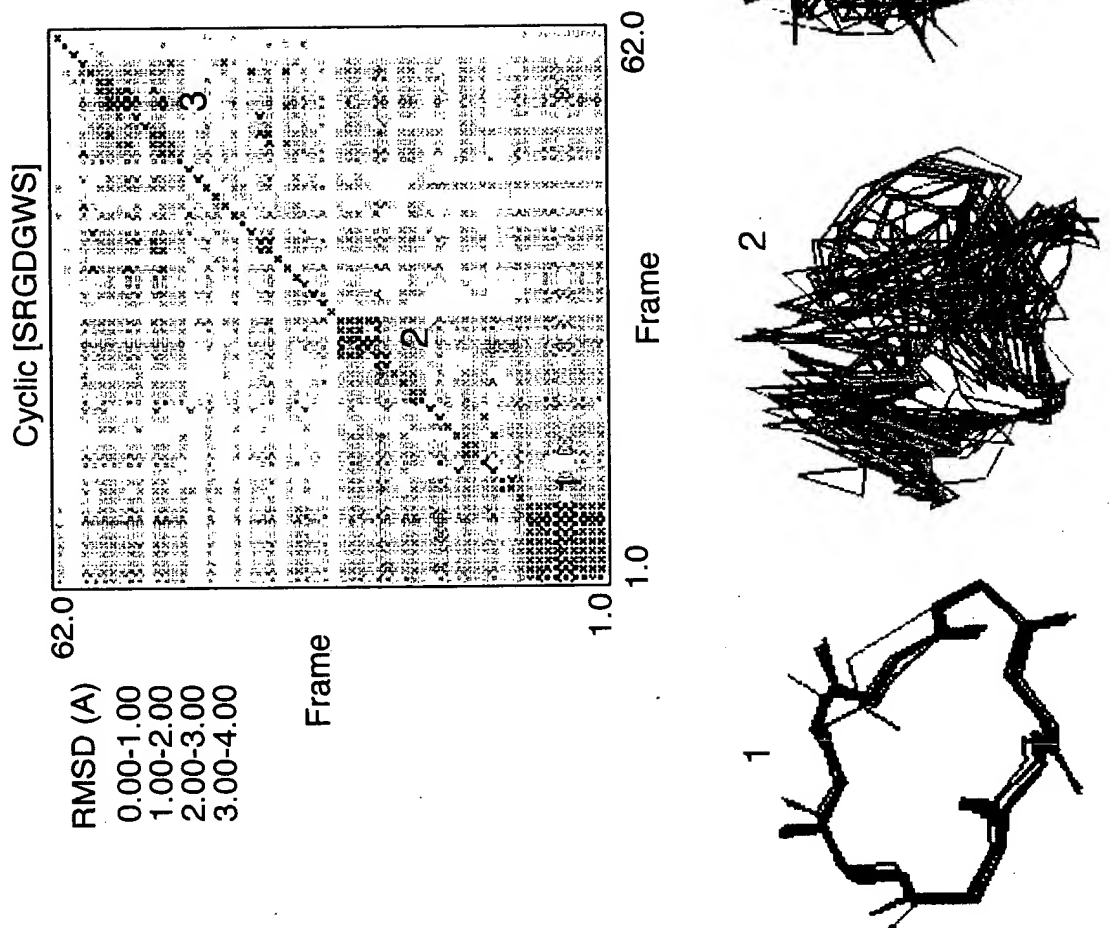


FIG._16

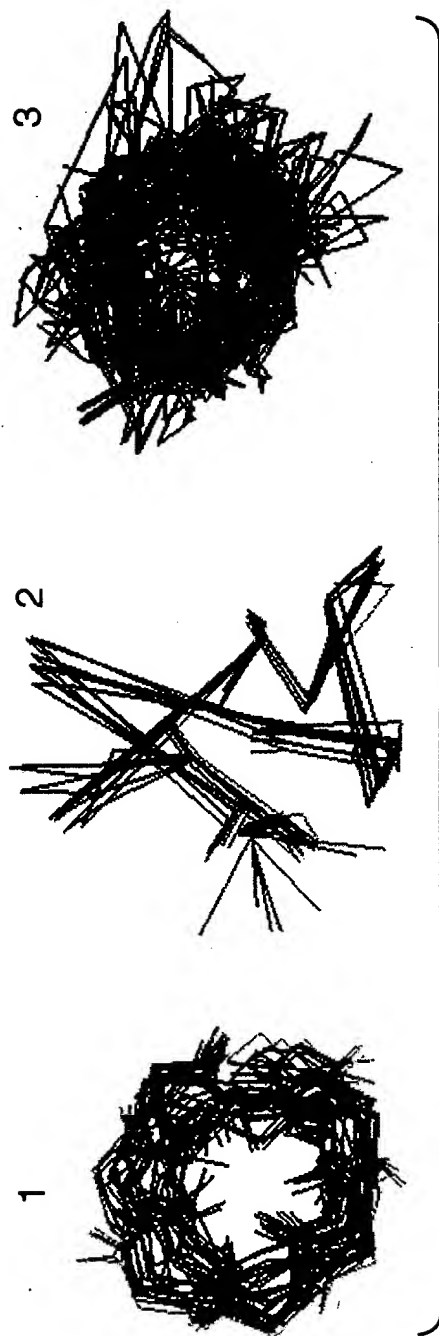
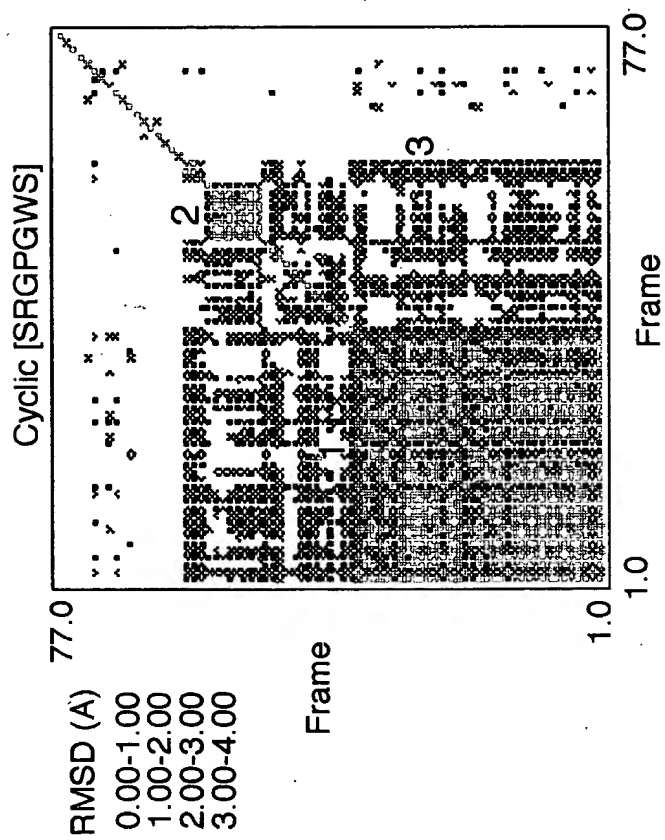


FIG._17